FIG. 1

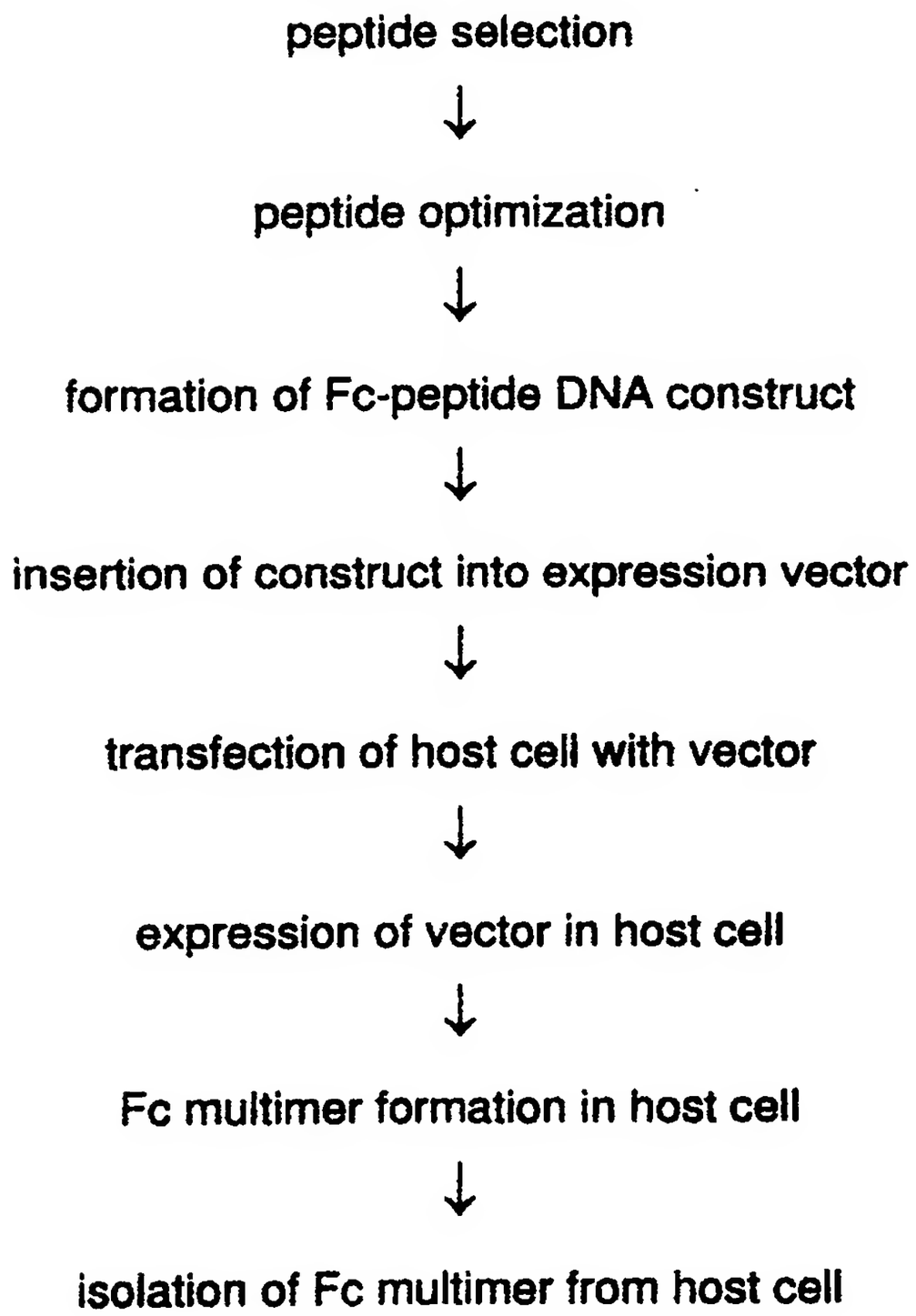

peptide selection
peptide optimization
formation of Fc-peptide DNA construct
insertion of construct into expression vector
transfection of host cell with vector
expression of vector in host cell
Fc multimer formation in host cell
isolation of Fc multimer from host cell

FIG. 2A

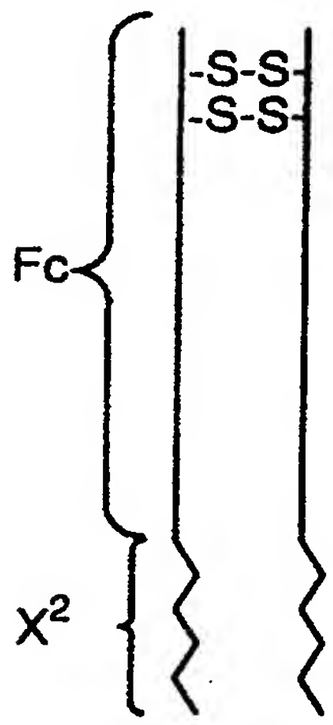


FIG. 2B

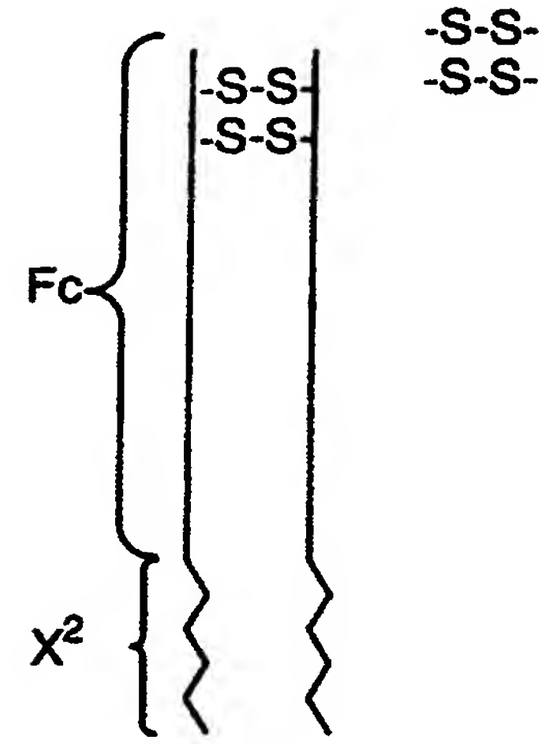


FIG. 2C

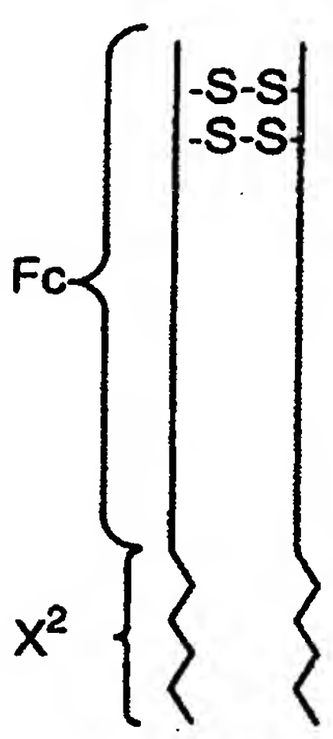


FIG. 2D

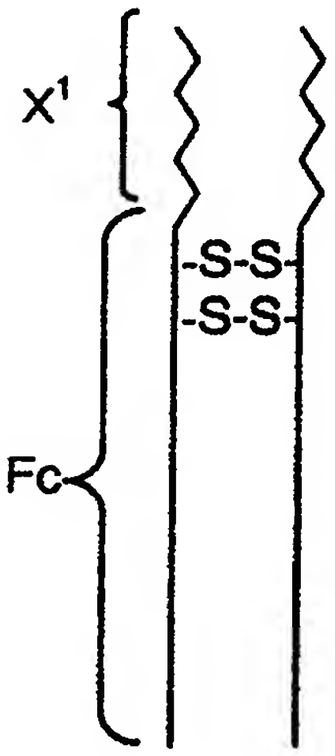


FIG. 2E

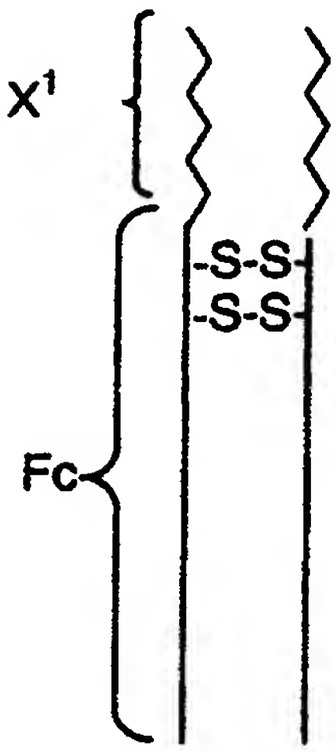


FIG. 2F

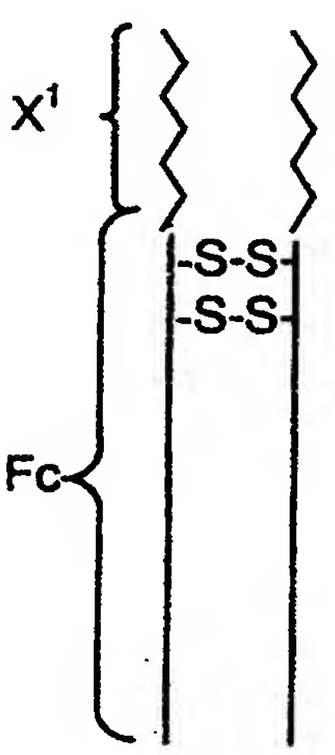


FIG. 3A

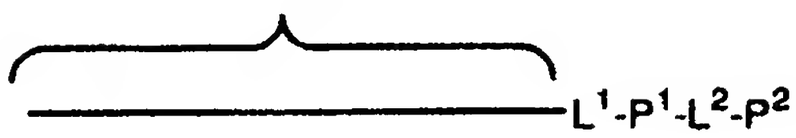


FIG. 3B

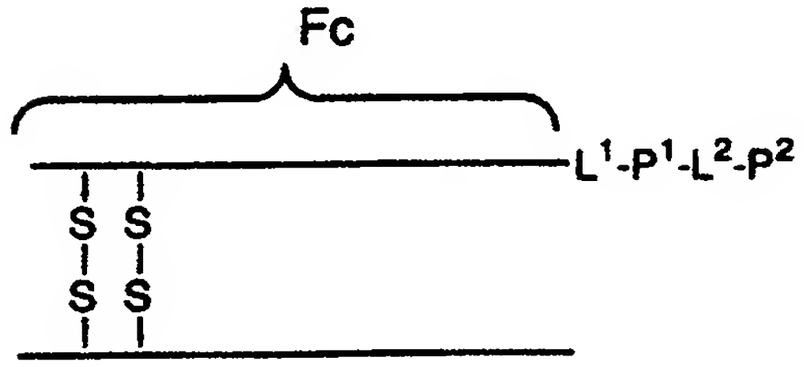


FIG. 3C

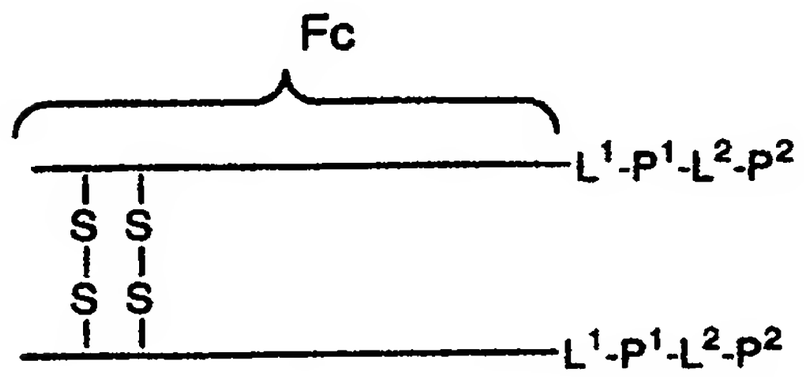


FIG. 4

```
                ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGGACCGTCA
              1 ---------+---------+---------+---------+---------+---------+-------- 60
                TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a                M  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S  -

                GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
             61 ---------+---------+---------+---------+---------+---------+-------- 120
                CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a                V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V  -

                ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
            121 ---------+---------+---------+---------+---------+---------+-------- 180
                TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a                T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  -

                GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
            181 ---------+---------+---------+---------+---------+---------+-------- 240
                CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a                D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  -

                TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
            241 ---------+---------+---------+---------+---------+---------+-------- 300
                ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG

a                Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  -

                AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
            301 ---------+---------+---------+---------+---------+---------+-------- 360
                TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a                K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A  -

                AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
            361 ---------+---------+---------+---------+---------+---------+-------- 420
                TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a                K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  T  -

                AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
            421 ---------+---------+---------+---------+---------+---------+-------- 480
                TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a                K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  -

                GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
            481 ---------+---------+---------+---------+---------+---------+-------- 540
                CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG

a                E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  -

                TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
            541 ---------+---------+---------+---------+---------+---------+-------- 600
                AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a                S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  -

                GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
            601 ---------+---------+---------+---------+---------+---------+-------- 660
                CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

a                G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  -

                AGCCTCTCCCTGTCTCCGGGTAAA
            661 ---------+---------+----  684
                TCGGAGAGGGACAGAGGCCCATTT
```

FIG. 5

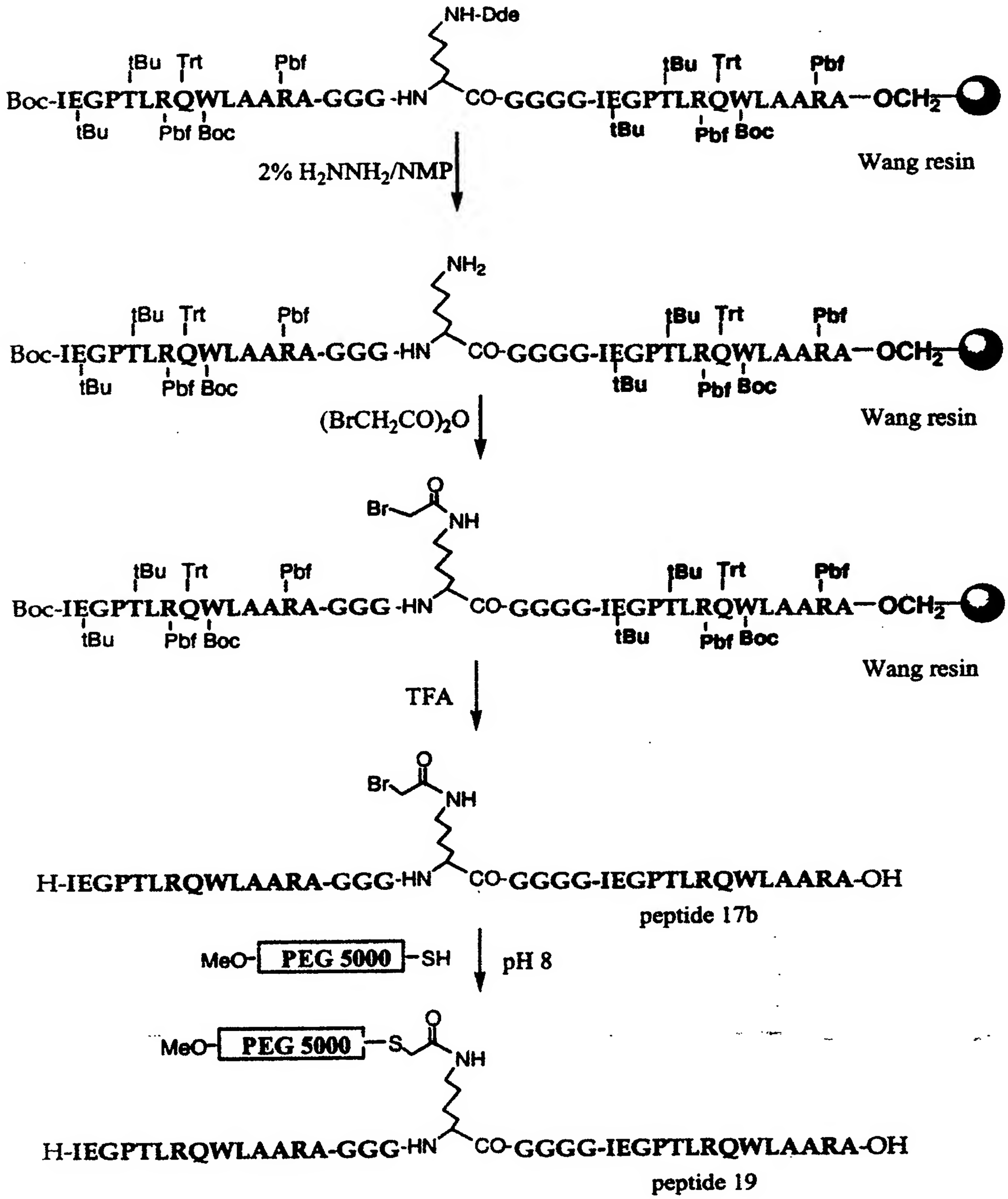

NH-Dde
tBu Trt Pbf
Boc-IEGPTLRQWLAARA-GGG-HN
CO-GGGG-IEGPTLRQWLAARA—OCH2
tBu Pbf Boc
Wang resin
2% H2NNH2/NMP
NH2
(BrCH2CO)2O
Br
O
NH
TFA
H-IEGPTLRQWLAARA-GGG-HN
CO-GGGG-IEGPTLRQWLAARA-OH
peptide 17b
MeO-PEG 5000-SH
pH 8
MeO-PEG 5000-S
peptide 19

FIG. 6

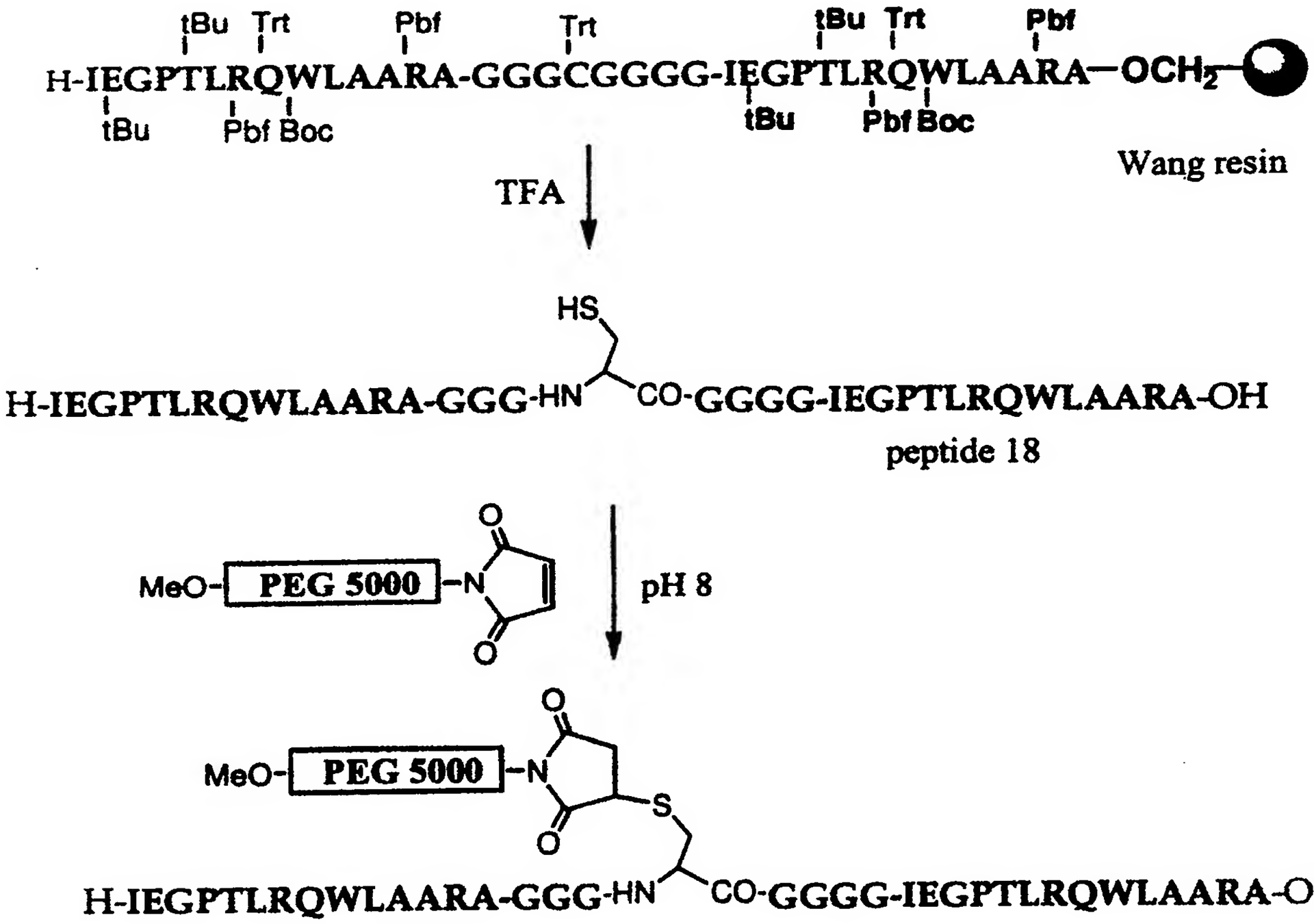

tBu Trt Pbf Trt tBu Trt Pbf
H-IEGPTLRQWLAARA-GGGCGGGG-IEGPTLRQWLAARA—OCH2
tBu Pbf Boc tBu Pbf Boc
Wang resin
TFA
HS
H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH
peptide 18
MeO- PEG 5000 -N
pH 8
MeO- PEG 5000 -N S
H-IEGPTLRQWLAARA-GGG-HN CO-GGGG-IEGPTLRQWLAARA-OH
peptide 20

FIG. 7

```
          XbaI
          |
          TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC
        1 ---------+---------+---------+---------+---------+---------+ 60
          AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
c                                                   M  D  K  T  H  T  C  P -

          CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
       61 ---------+---------+---------+---------+---------+---------+ 120
          GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
c           P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P -

          CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
      121 ---------+---------+---------+---------+---------+---------+ 180
          GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
c           K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S -

          GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
      181 ---------+---------+---------+---------+---------+---------+ 240
          CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
c           H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A -

          CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
      241 ---------+---------+---------+---------+---------+---------+ 300
          GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
c           K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T -

          CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
      301 ---------+---------+---------+---------+---------+---------+ 360
          GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
c           V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A -

          CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
      361 ---------+---------+---------+---------+---------+---------+ 420
          GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
c           L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q -

          AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
      421 ---------+---------+---------+---------+---------+---------+ 480
          TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
c           V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C -

          GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
      481 ---------+---------+---------+---------+---------+---------+ 540
          CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
c           L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P -

          CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
      541 ---------+---------+---------+---------+---------+---------+ 600
          GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
c           E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y -

          ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
      601 ---------+---------+---------+---------+---------+---------+ 660
          TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
c           S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V -

          TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
      661 ---------+---------+---------+---------+---------+---------+ 720
          ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
c           M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K -

          AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTT
      721 ---------+---------+---------+---------+---------+---------+ 780
          TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAA
c           G  G  G  G  G  I  E  G  P  T  L  R  Q  W  L  A  A  R  A  * -

              BamHI
              |
          AATCTCGAGGATCC
      781 ---------+---- 794
          TTAGAGCTCCTAGG
```

FIG. 8

```
          XbaI
            |
            TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC
          1 ---------+---------+---------+---------+---------+---------+---------+ 60
            AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
c                                                    M  D  K  T  H  T  C  P  -

            CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
         61 ---------+---------+---------+---------+---------+---------+---------+ 120
            GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
c             P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  -

            CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
        121 ---------+---------+---------+---------+---------+---------+---------+ 180
            GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
c             K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  -

            GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
        181 ---------+---------+---------+---------+---------+---------+---------+ 240
            CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
c             H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  -

            CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
        241 ---------+---------+---------+---------+---------+---------+---------+ 300
            GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
c             K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  -

            CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
        301 ---------+---------+---------+---------+---------+---------+---------+ 360
            GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
c             V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  -

            CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
        361 ---------+---------+---------+---------+---------+---------+---------+ 420
            GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
c             L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  -

            AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
        421 ---------+---------+---------+---------+---------+---------+---------+ 480
            TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
c             V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  -

            GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
        481 ---------+---------+---------+---------+---------+---------+---------+ 540
            CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
c             L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  -

            CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
        541 ---------+---------+---------+---------+---------+---------+---------+ 600
            GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
c             E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  -

            ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
        601 ---------+---------+---------+---------+---------+---------+---------+ 660
            TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
c             S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  -

            TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
        661 ---------+---------+---------+---------+---------+---------+---------+ 720
            ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
c             M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  -

            AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTG
        721 ---------+---------+---------+---------+---------+---------+---------+ 780
            TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAC
c             G  G  G  G  G  I  E  G  P  T  L  R  Q  W  L  A  A  R  A  G  -

            GTGGTGGAGGTGGCGGCGGAGGTATTGAGGGCCCAACCCTTCGCCAATGGCTTGCAGCAC
        781 ---------+---------+---------+---------+---------+---------+---------+ 840
            CACCACCTCCACCGCCGCCTCCATAACTCCCGGGTTGGGAAGCGGTTACCGAACGTCGTG
c             G  G  G  G  G  G  G  I  E  G  P  T  L  R  Q  W  L  A  A  R  -

                        BamHI
                          |
            GCGCATAATCTCGAGGATCCG
        841 ---------+---------+- 861
            CGCGTATTAGAGCTCCTAGGC
                                c           A  *  -
```

FIG. 9

```
          XbaI
           |
           TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
         1 ---------+---------+---------+---------+---------+---------+---------+ 60
           AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
c                                                  M  I  E  G  P  T  L  R -

           GTCAGTGGCTGGCTGCTCGTGCTGGCGGTGGTGGCGGAGGGGGTGGCATTGAGGGCCCAA
        61 ---------+---------+---------+---------+---------+---------+---------+ 120
           CAGTCACCGACCGACGAGCACGACCGCCACCACCGCCTCCCCCACCGTAACTCCCGGGTT
c            Q  W  L  A  A  R  A  G  G  G  G  G  G  G  G  I  E  G  P  T -

           CCCTTCGCCAATGGCTTGCAGCACGCGCAGGGGGAGGCGGTGGGGACAAAACTCACACAT
       121 ---------+---------+---------+---------+---------+---------+---------+ 180
           GGGAAGCGGTTACCGAACGTCGTGCGCGTCCCCCTCCGCCACCCCTGTTTTGAGTGTGTA
c            L  R  Q  W  L  A  A  R  A  G  G  G  G  G  D  K  T  H  T  C -

           GTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAA
       181 ---------+---------+---------+---------+---------+---------+---------+ 240
           CAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTT
c            P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K -

           AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACG
       241 ---------+---------+---------+---------+---------+---------+---------+ 300
           TTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGC
c            P  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V -

           TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATA
       301 ---------+---------+---------+---------+---------+---------+---------+ 360
           ACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTAT
c            S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N -

           ATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
       361 ---------+---------+---------+---------+---------+---------+---------+ 420
           TACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGG
c            A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L -

           TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
       421 ---------+---------+---------+---------+---------+---------+---------+ 480
           AGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGT
c            T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K -

           AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
       481 ---------+---------+---------+---------+---------+---------+---------+ 540
           TTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTG
c            A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P -

           CACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGA
       541 ---------+---------+---------+---------+---------+---------+---------+ 600
           GTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACT
c            Q  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T -

           CCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC
       601 ---------+---------+---------+---------+---------+---------+---------+ 660
           GGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCG
c            C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q -

           AGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCC
       661 ---------+---------+---------+---------+---------+---------+---------+ 720
           TCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGG
c            P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L -

           TCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT
       721 ---------+---------+---------+---------+---------+---------+---------+ 780
           AGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGA
c            Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S -

           CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
       781 ---------+---------+---------+---------+---------+---------+---------+ 840
           GGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCC
c            V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G -

                BamHI
                  |
           GTAAATAATGGATCC
       841 ---------+----- 855
           CATTTATTACCTAGG
c            K  *
```

FIG. 10

```
          XbaI
           |
           TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC
         1 ---------+---------+---------+---------+---------+---------+---------+ 60
           AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG
c                                                    M  I  E  G  P  T  L  R  -

           GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCGGTGGGGACAAAACTCACACATGTCCAC
        61 ---------+---------+---------+---------+---------+---------+---------+ 120
           CAGTCACCGACCGACGAGCACGACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG
c            Q  W  L  A  A  R  A  G  G  G  G  G  D  K  T  H  T  C  P  P  -

           CTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCA
       121 ---------+---------+---------+---------+---------+---------+---------+ 180
           GAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGT
c            C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  -

           AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC
       181 ---------+---------+---------+---------+---------+---------+---------+ 240
           TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG
c            D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  -

           ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA
       241 ---------+---------+---------+---------+---------+---------+---------+ 300
           TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT
c            E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  -

           AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCG
       301 ---------+---------+---------+---------+---------+---------+---------+ 360
           TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC
c            T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  -

           TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
       361 ---------+---------+---------+---------+---------+---------+---------+ 420
           AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG
c            L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  -

           TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
       421 ---------+---------+---------+---------+---------+---------+---------+ 480
           AGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC
c            P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  V  -

           TGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC
       481 ---------+---------+---------+---------+---------+---------+---------+ 540
           ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG
c            Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  L  -

           TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
       541 ---------+---------+---------+---------+---------+---------+---------+ 600
           ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCC
c            V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  E  -

           AGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACA
       601 ---------+---------+---------+---------+---------+---------+---------+ 660
           TCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGT
c            N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  -

           GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
       661 ---------+---------+---------+---------+---------+---------+---------+ 720
           CGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACT
c            K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  -

           TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT
       721 ---------+---------+---------+---------+---------+---------+---------+ 780
           ACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA
c            H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  *  -

            BamHI
             |
           AATGGATCC
       781 --------- 789
           TTACCTAGG
```

FIG.11

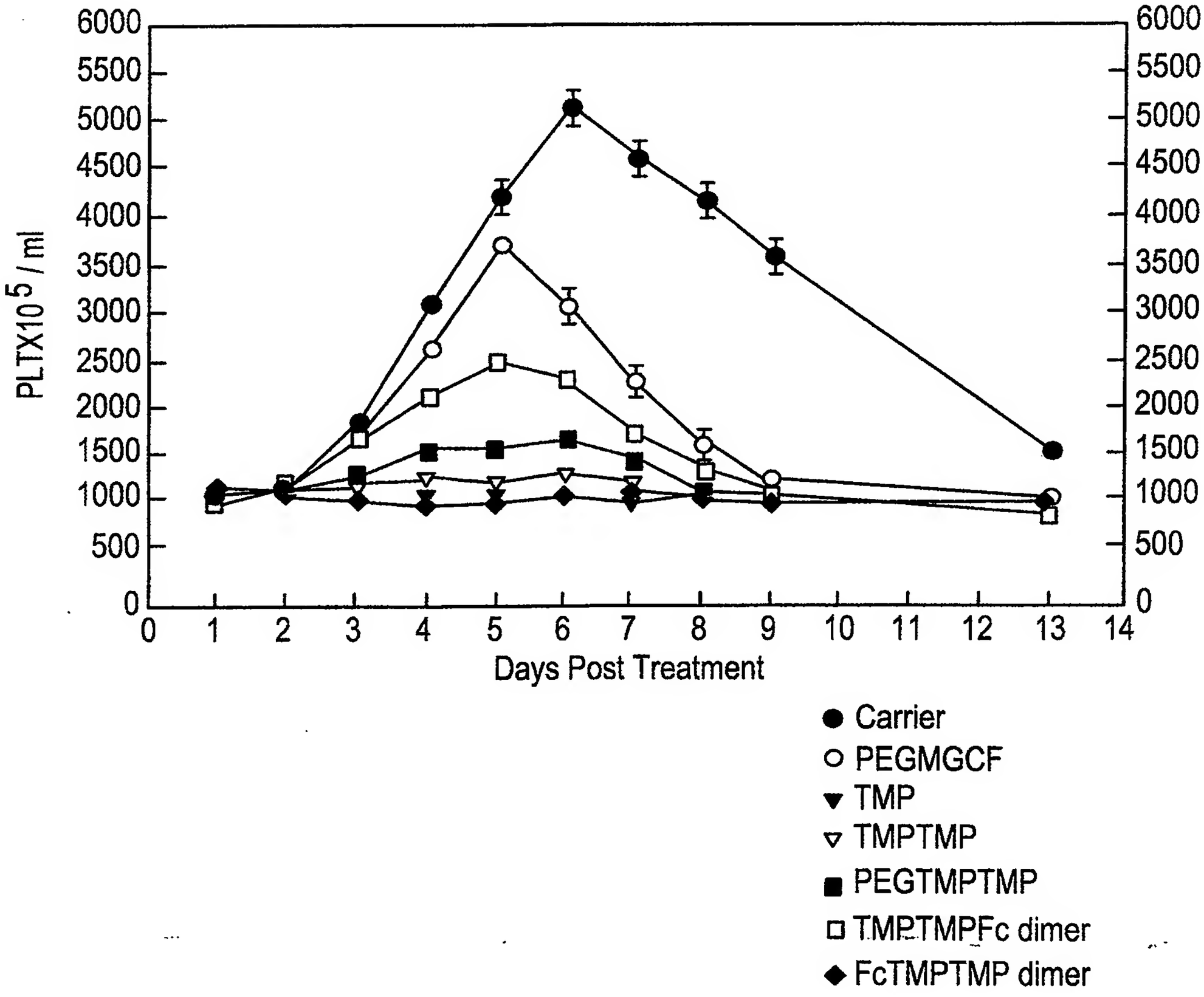

PLTX10^5/ml
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days Post Treatment
Carrier
PEGMGCF
TMP
TMPTMP
PEGTMPTMP
TMPTMPFc dimer
FcTMPTMP dimer

FIG.12

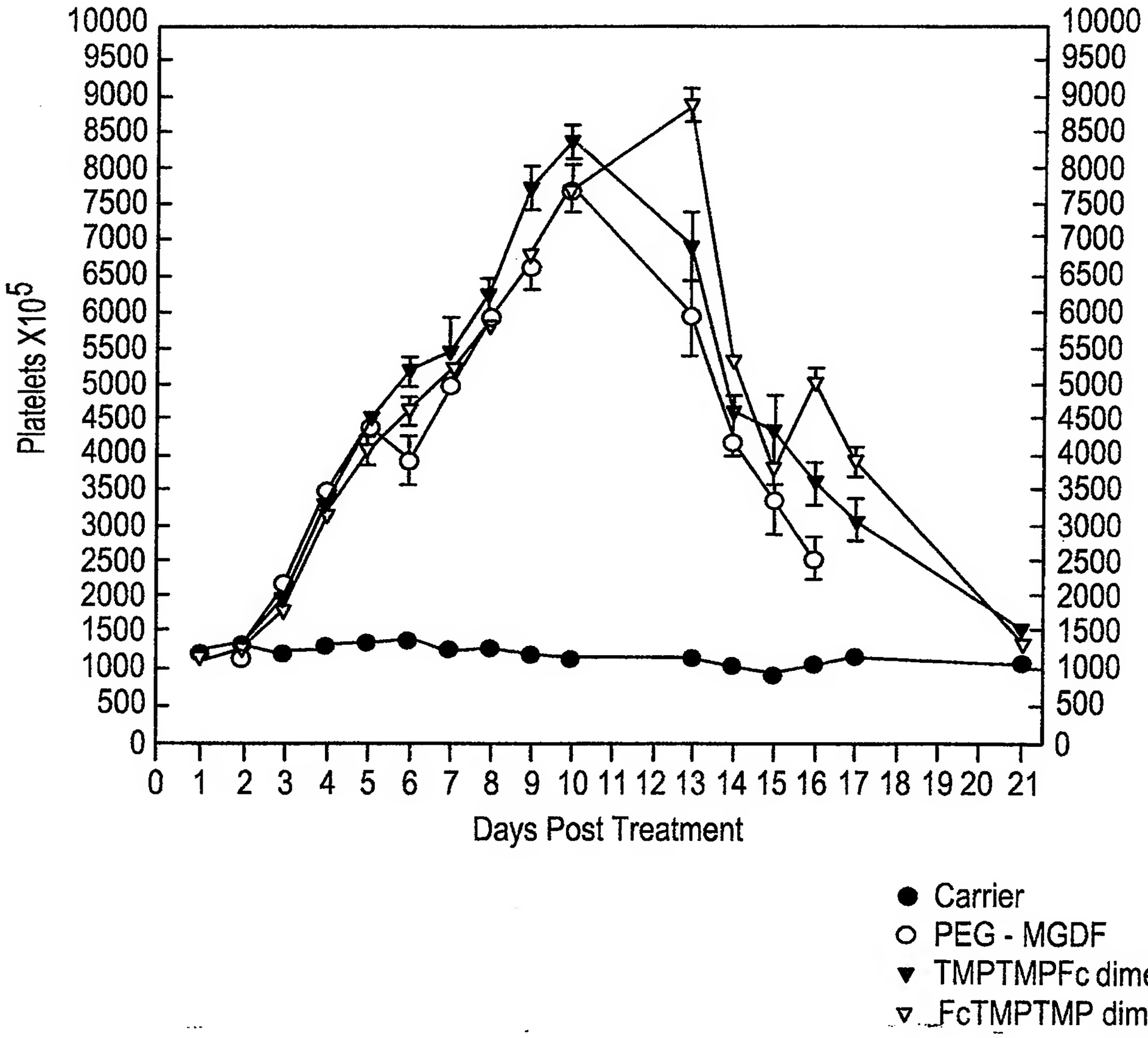

Platelets X10^5
10000
9500
9000
8500
8000
7500
7000
6500
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
Days Post Treatment
Carrier
PEG - MGDF
TMPTMPFc dimer
FcTMPTMP dimer

FIG. 13

```
                XbaI
                 |
                TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC
              1 ---------+---------+---------+---------+---------+---------+---------+ 60
                AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
C                                                     M  D  K  T  H  T  C  P  -
                CACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAAC
             61 ---------+---------+---------+---------+---------+---------+---------+ 120
                GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG
C                  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  -

                CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
            121 ---------+---------+---------+---------+---------+---------+---------+ 180
                GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
C                  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  -

                GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
            181 ---------+---------+---------+---------+---------+---------+---------+ 240
                CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
C                  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  -

                CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
            241 ---------+---------+---------+---------+---------+---------+---------+ 300
                GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
C                  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  -

                CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
            301 ---------+---------+---------+---------+---------+---------+---------+ 360
                GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
C                  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  -

              CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
            361 ---------+---------+---------+---------+---------+---------+---------+ 420
                GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
C                  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  -

                AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
            421 ---------+---------+---------+---------+---------+---------+---------+ 480
                TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
C                  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  -

                GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
            481 ---------+---------+---------+---------+---------+---------+---------+ 540
                CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
C                  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  -
                CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
            541 ---------+---------+---------+---------+---------+---------+---------+ 600
                GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
C                  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  -

                ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
            601 ---------+---------+---------+---------+---------+---------+---------+ 660
                TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
C                  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  -

                TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
            661 ---------+---------+---------+---------+---------+---------+---------+ 720
                ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
C                  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  -

                AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT
            721 ---------+---------+---------+---------+---------+---------+---------+ 780
                TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA
C                  G  G  G  G  G  G  G  T  Y  S  C  H  F  G  P  L  T  W  V  C  -

                                                BamHI
                                                 |
                GCAAACCGCAGGGTGGTTAATCTCGTGGATCC
            781 ---------+---------+---------+-- 812
                CGTTTGGCGTCCCACCAATTAGAGCACCTAGG
C                  K  P  Q  G  G  *
```

FIG. 14

```
          XbaI
           |
           TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC
         1 ---------+---------+---------+---------+---------+---------+ 60
           AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCCTCCATGAATGAGAACGG
c                                                   M  G  G  T  Y  S  C  H  -

           ACTTCGGCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGGACA
        61 ---------+---------+---------+---------+---------+---------+ 120
           TGAAGCCGGGCGACTGAACCCATACATTCGGTGTTCCCCCACCCCCTCCGCCCCCCCTGT
c            F  G  P  L  T  W  V  C  K  P  Q  G  G  G  G  G  G  G  D  K  -

           AAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCC
       121 ---------+---------+---------+---------+---------+---------+ 180
           TTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGG
c            T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  -

           TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
       181 ---------+---------+---------+---------+---------+---------+ 240
           AGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGC
c            F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  -

           TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG
       241 ---------+---------+---------+---------+---------+---------+ 300
           ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
c            V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  -

           TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
       301 ---------+---------+---------+---------+---------+---------+ 360
           ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC
c            E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  -

           TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
       361 ---------+---------+---------+---------+---------+---------+ 420
           ACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGT
c            V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  -

           AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
       421 ---------+---------+---------+---------+---------+---------+ 480
           TCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG
c            V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  -

           AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC
       481 ---------+---------+---------+---------+---------+---------+ 540
           TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGGTAGGGCCCTACTCGACTGGTTCTTGG
c            P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  -

           AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
       541 ---------+---------+---------+---------+---------+---------+ 600
           TCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC
c            V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  -

           AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
       601 ---------+---------+---------+---------+---------+---------+ 660
           TCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGC
c            S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  -

           GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
       661 ---------+---------+---------+---------+---------+---------+ 720
           CGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGC
c            S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  -

           TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
       721 ---------+---------+---------+---------+---------+---------+ 780
           AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA
c            F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  -

                                  BamHI
                                    |
           CCCTGTCTCCGGGTAAATAATGGATCC
       781 ---------+---------+------- 807
           GGGACAGAGGCCCATTTATTACCTAGG
c            L  S  P  G  K  *
```

FIG. 15

```
          XbaI
            |
            TCTAGATTTGAGTTTTAACTTTTAGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG
          1 ---------+---------+---------+---------+---------+---------+---------+ 60
            AGATCTAAACTCAAAATTGAAAATCTTCCTCCTTATTTTATACCCTCCATGAATGAGAAC
b                                                   M   G   G   T   Y   S   C   -

            CCACTTCGGCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGG
         61 ---------+---------+---------+---------+---------+---------+---------+ 120
            GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCCACCGCCGCCGCCGCCGCCACC
b             H   F   G   P   L   T   W   V   C   K   P   Q   G   G   G   G   G   G   G   G   -

            TACCTATTCCTGTCATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGG
        121 ---------+---------+---------+---------+---------+---------+---------+ 180
            ATGGATAAGGACAGTAAAACCGGGCGACTGGACCCATACATTCGGTGTTCCCCCACCCCC
b             T   Y   S   C   H   F   G   P   L   T   W   V   C   K   P   Q   G   G   G   G   -

            AGGCGGGGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGG
        181 ---------+---------+---------+---------+---------+---------+---------+ 240
            TCCGCCCCCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCC
b             G   G   G   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   -

            ACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
        241 ---------+---------+---------+---------+---------+---------+---------+ 300
            TGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGG
b             P   S   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   -

            TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG
        301 ---------+---------+---------+---------+---------+---------+---------+ 360
            ACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC
b             E   V   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   -

            GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA
        361 ---------+---------+---------+---------+---------+---------+---------+ 420
            CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTT
b             Y   V   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   -

            CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA
        421 ---------+---------+---------+---------+---------+---------+---------+ 480
            GTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTT
b             S   T   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   -

            GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
        481 ---------+---------+---------+---------+---------+---------+---------+ 540
            CCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAG
b             E   Y   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   -

            CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA
        541 ---------+---------+---------+---------+---------+---------+---------+ 600
            GTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACT
b             K   A   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   -

            GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
        601 ---------+---------+---------+---------+---------+---------+---------+ 660
            CGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTA
b             L   T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   -

            CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT
        661 ---------+---------+---------+---------+---------+---------+---------+ 720
            GCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCA
b             A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   -

            GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
        721 ---------+---------+---------+---------+---------+---------+---------+ 780
            CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCAC
b             L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V   D   K   S   R   W   -

            GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
        781 ---------+---------+---------+---------+---------+---------+---------+ 840
            CGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTG
b             Q   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   -

                                                BamHI
                                                  |
            GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
        841 ---------+---------+---------+---------+-- 881
            CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
b             Q   K   S   L   S   L   S   P   G   K   *
```

FIG. 16

```
                XbaI
                 |
                TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC
          1     ---------+---------+---------+---------+---------+---------+     60
                AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
c                                                       M  D  K  T  H  T  C  P  -

                CACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAAC
         61     ---------+---------+---------+---------+---------+---------+    120
                GTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTG
c                 P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  -

                CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
        121     ---------+---------+---------+---------+---------+---------+    180
                GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
c                 K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  -

                GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
        181     ---------+---------+---------+---------+---------+---------+    240
                CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
c                 H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  -

                CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
        241     ---------+---------+---------+---------+---------+---------+    300
                GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
c                 K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  -

                CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
        301     ---------+---------+---------+---------+---------+---------+    360
                GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
c                 V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  -

                CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
        361     ---------+---------+---------+---------+---------+---------+    420
                GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
c                 L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  -

                AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
        421     ---------+---------+---------+---------+---------+---------+    480
                TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
c                 V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  -

                GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
        481     ---------+---------+---------+---------+---------+---------+    540
                CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
c                 L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  -

                CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
        541     ---------+---------+---------+---------+---------+---------+    600
                GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
c                 E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  -

                ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
        601     ---------+---------+---------+---------+---------+---------+    660
                TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
c                 S  K  L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  -

                TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
        661     ---------+---------+---------+---------+---------+---------+    720
                ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
c                 M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  -

                AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT
        721     ---------+---------+---------+---------+---------+---------+    780
                TTCCACCTCCACCACCGCCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA
c                 G  G  G  G  G  G  G  T  Y  S  C  H  F  G  P  L  T  W  V  C  -

                GCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGGTACCTATTCCTGTCATTTTGGCCCGC
        781     ---------+---------+---------+---------+---------+---------+    840
                CGTTTGGCGTCCCACCGCCGCCGCCGCCGCCACCATGGATAAGGACAGTAAAACCGGGCG
c                 K  P  Q  G  G  G  G  G  G  G  G  T  Y  S  C  H  F  G  P  L  -

                                                        BamHI
                                                         |
                TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC
        841     ---------+---------+---------+---------+----  884
                ACTGGACCCATACATTCGGTGTTCCCCCAATTAGAGCTCCTAGG
c                 T  W  V  C  K  P  Q  G  G  *
```

FIG. 17A

```
[AatII sticky end]                    5'     GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21)            3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA-

-GGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG-

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCTCCCACCGCCCGTCCTGCGGGCG-

-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT-
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-

                                                    AatII
-TTCTACAAACTCTTTTGTTTATTTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC-
-AAAATTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-

-GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCCTTCGCATGCCCACGCTAAAC-
-ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-

-ATTCTTTTTCTCTTTTGGTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTTC-
-TAAGAAAAAGAGAAAACCAATTTAGCAACAAACTAAATAATAAACGATATAAATAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTCATACACGCATGTAAAAATA-
-CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-

-AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAAACTAAGCATTCCGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA-

-TAGCAGTATGAATAGGGAAACTAAACCCAGTGATAAGACCTGATGATTTCGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-

-TTACATTTGGAGATTTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-

-AATATTGCCTCCATTTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACTTTATAGTCTAAATTGGTATC-

-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAAATCAGTATAGTC-

-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-
-TATTCGTAACTAATTATAGTAATAACGAAGATGTCCGAAATTAAAATAATTAATAAGACA-

-AAGTGTCGTCGGCATTTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-

-GCAAGTTTTGCGTGTTATATATCATTAAAACGGTAATAGATTGACATTTGATTCTAATAA-
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-
```

FIG. 17B

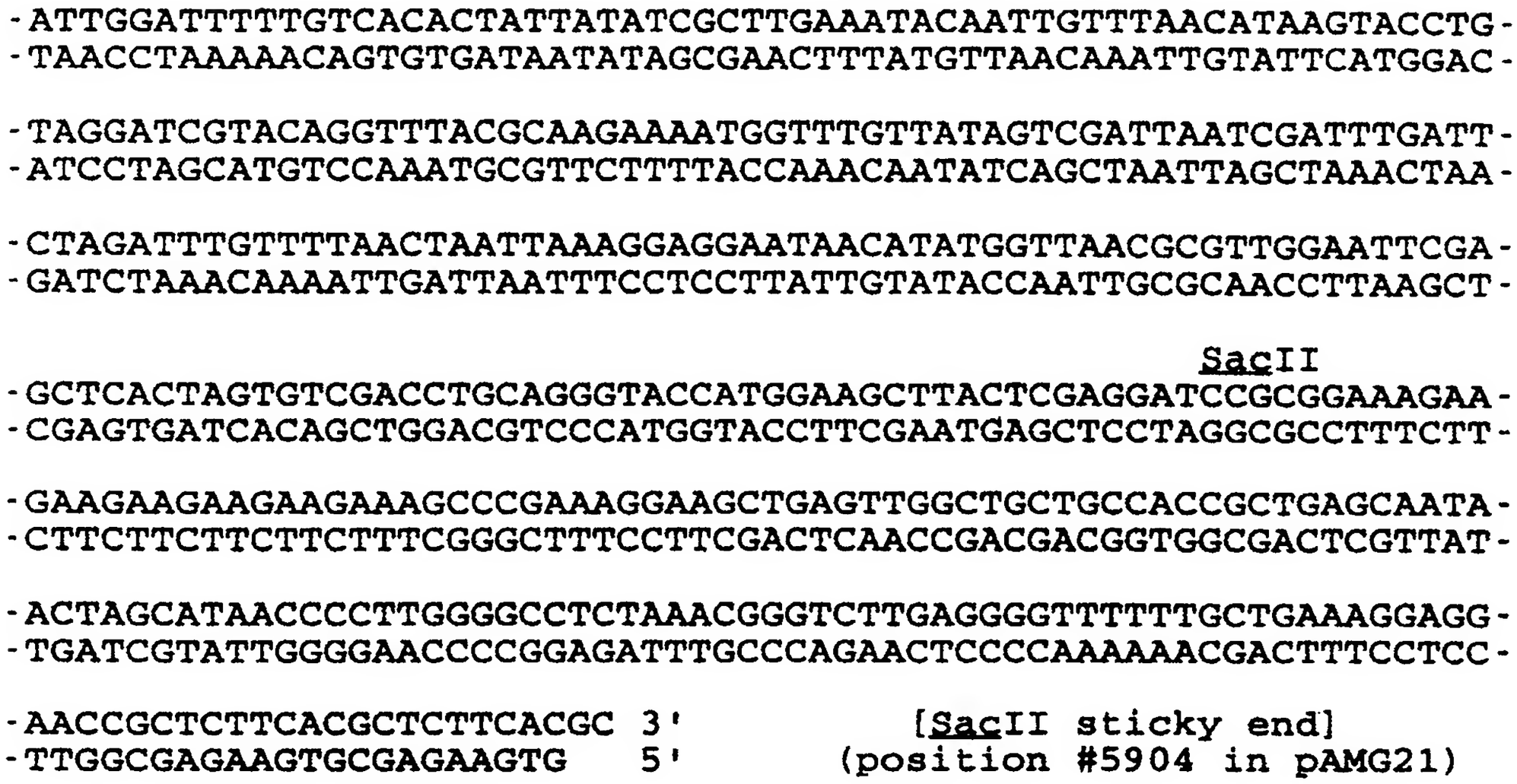

-ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG-
-TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC-
-TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGATTAATCGATTTGATT-
-ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA-
-CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA-
-GATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT-
SacII
-GCTCACTAGTGTCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA-
-CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT-
-GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA-
-CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT-
-ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGG-
-TGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAAACGACTTTCCTCC-
-AACCGCTCTTCACGCTCTTCACGC 3'
-TTGGCGAGAAGTGCGAGAAGTG 5'
[SacII sticky end]
(position #5904 in pAMG21)

FIG.18A - 1

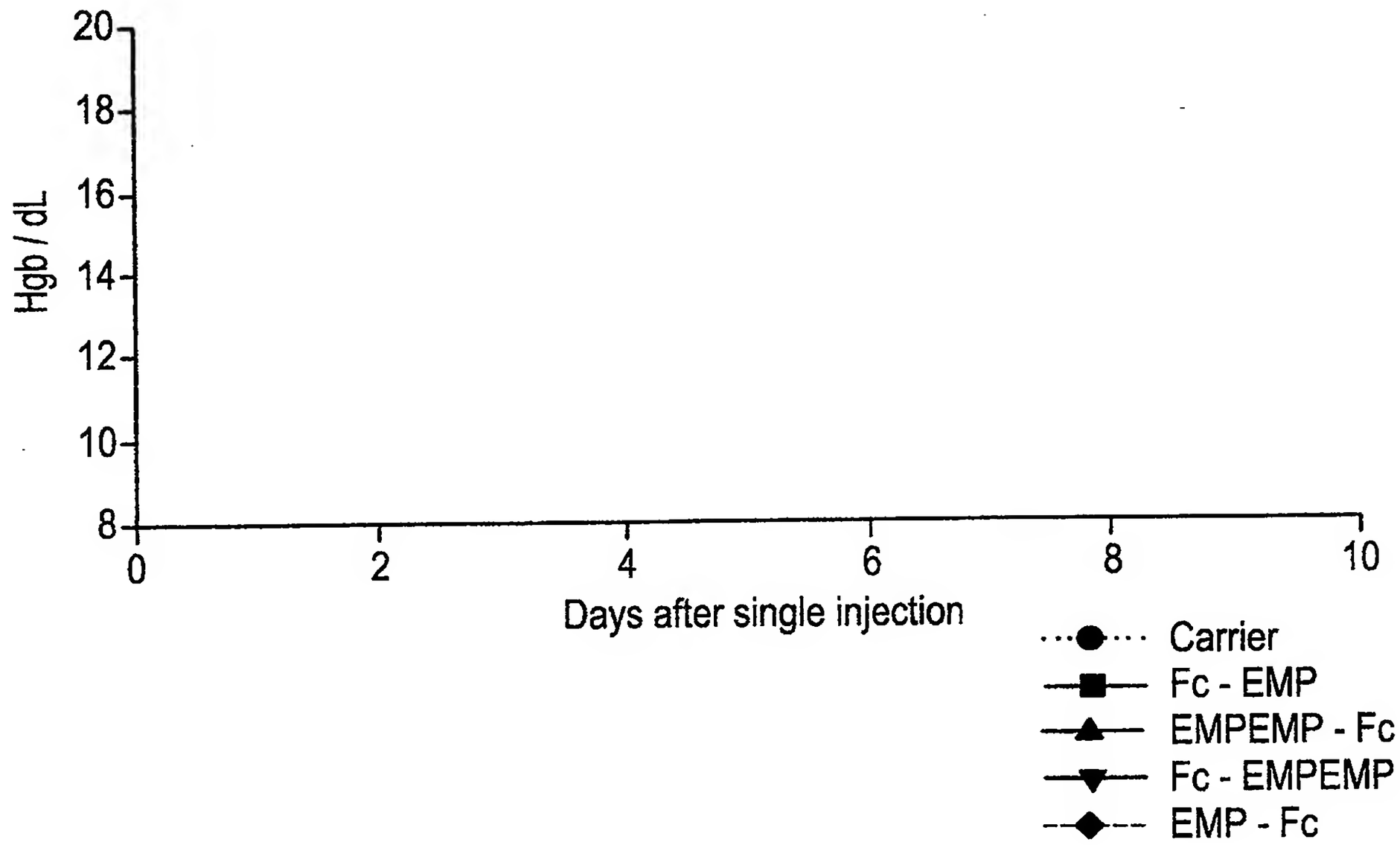


FIG.18A - 2

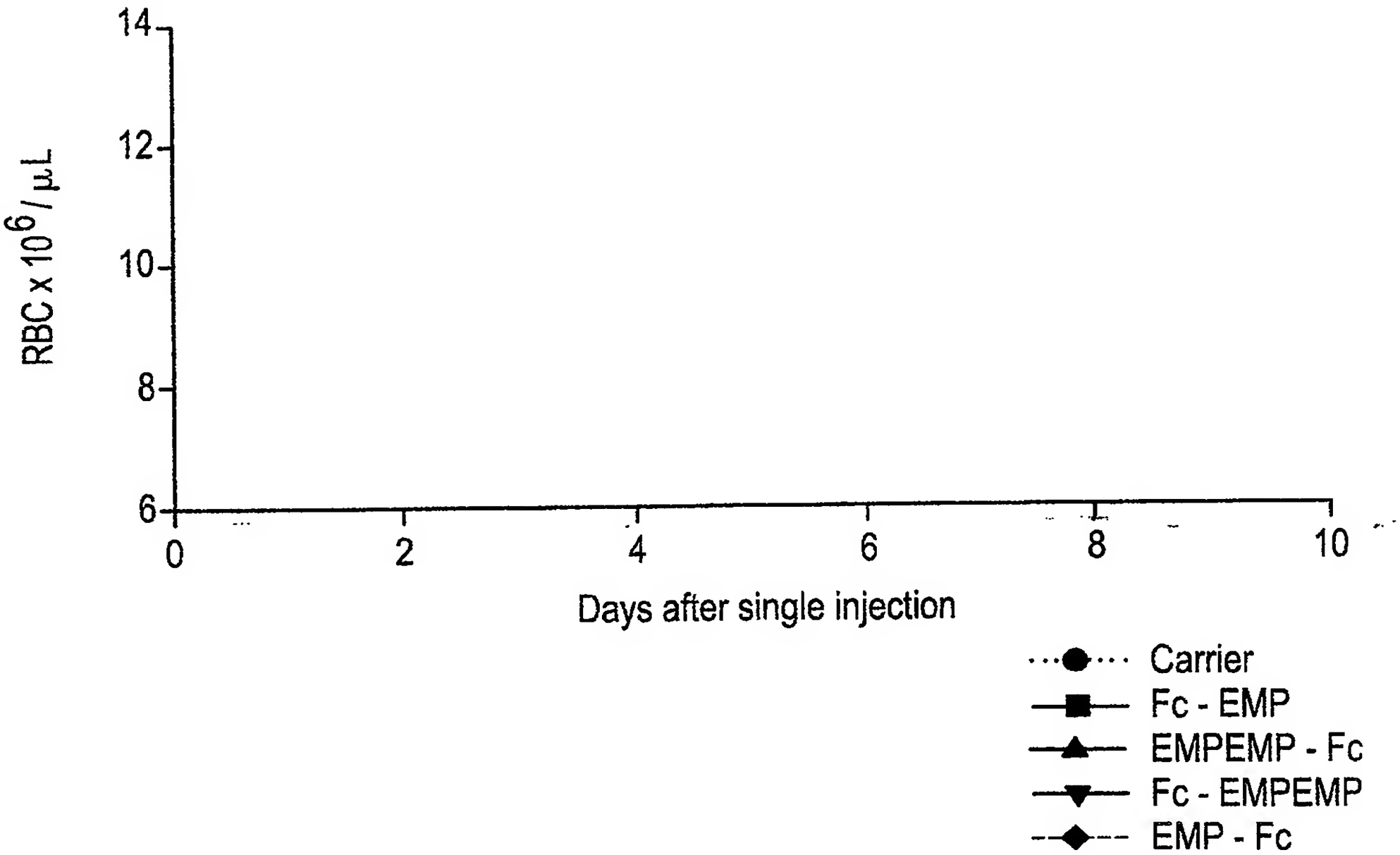


FIG.18A - 3

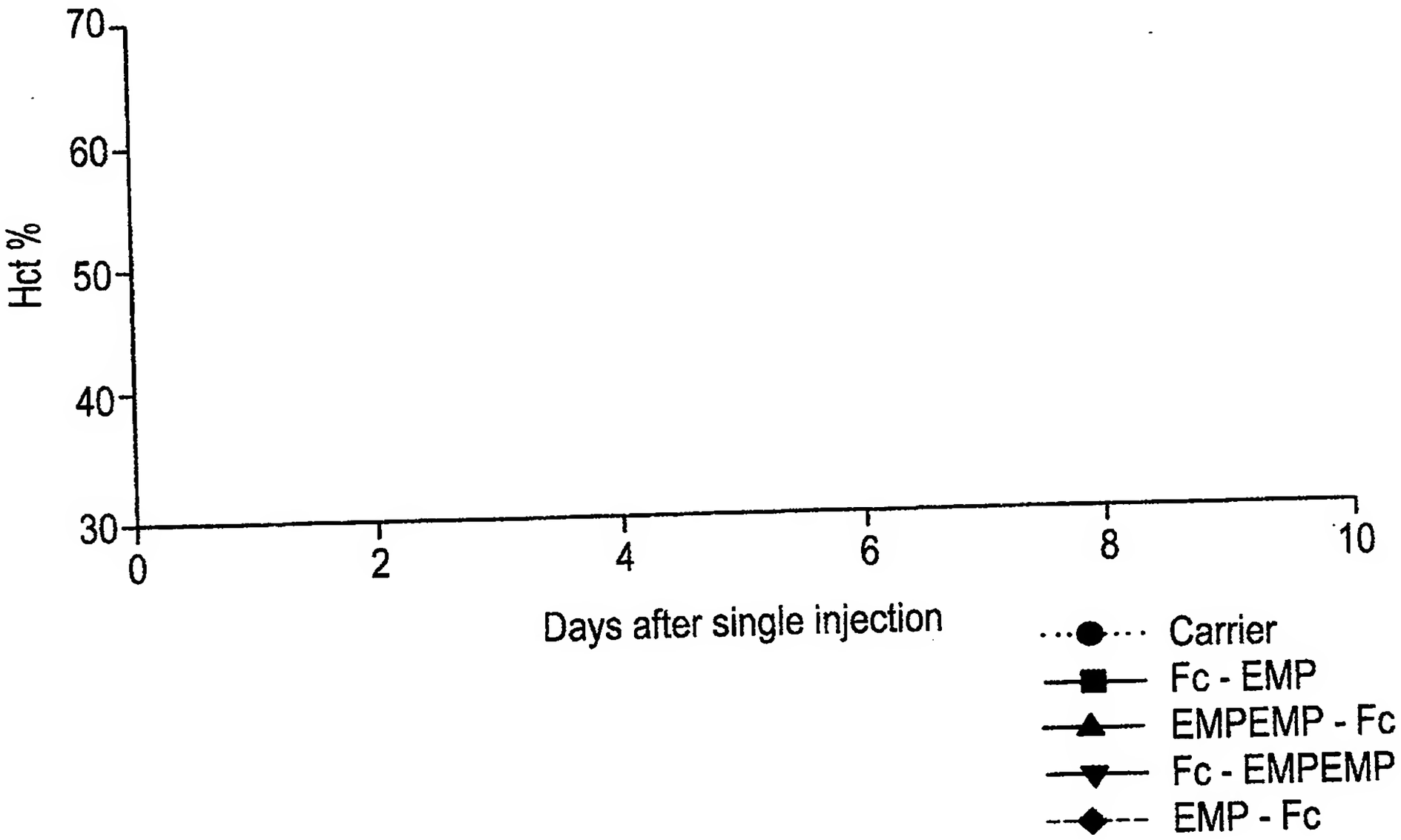


FIG.18B - 1

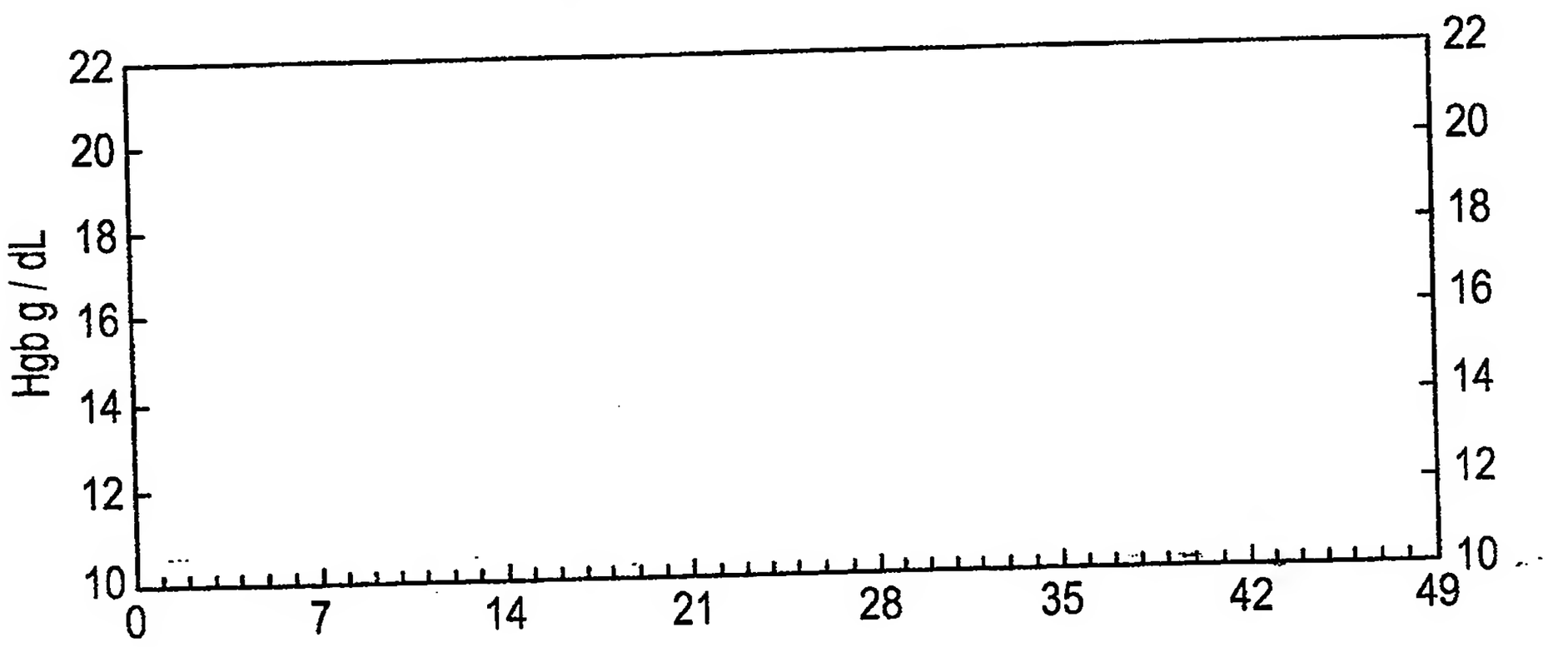


FIG.18B - 2

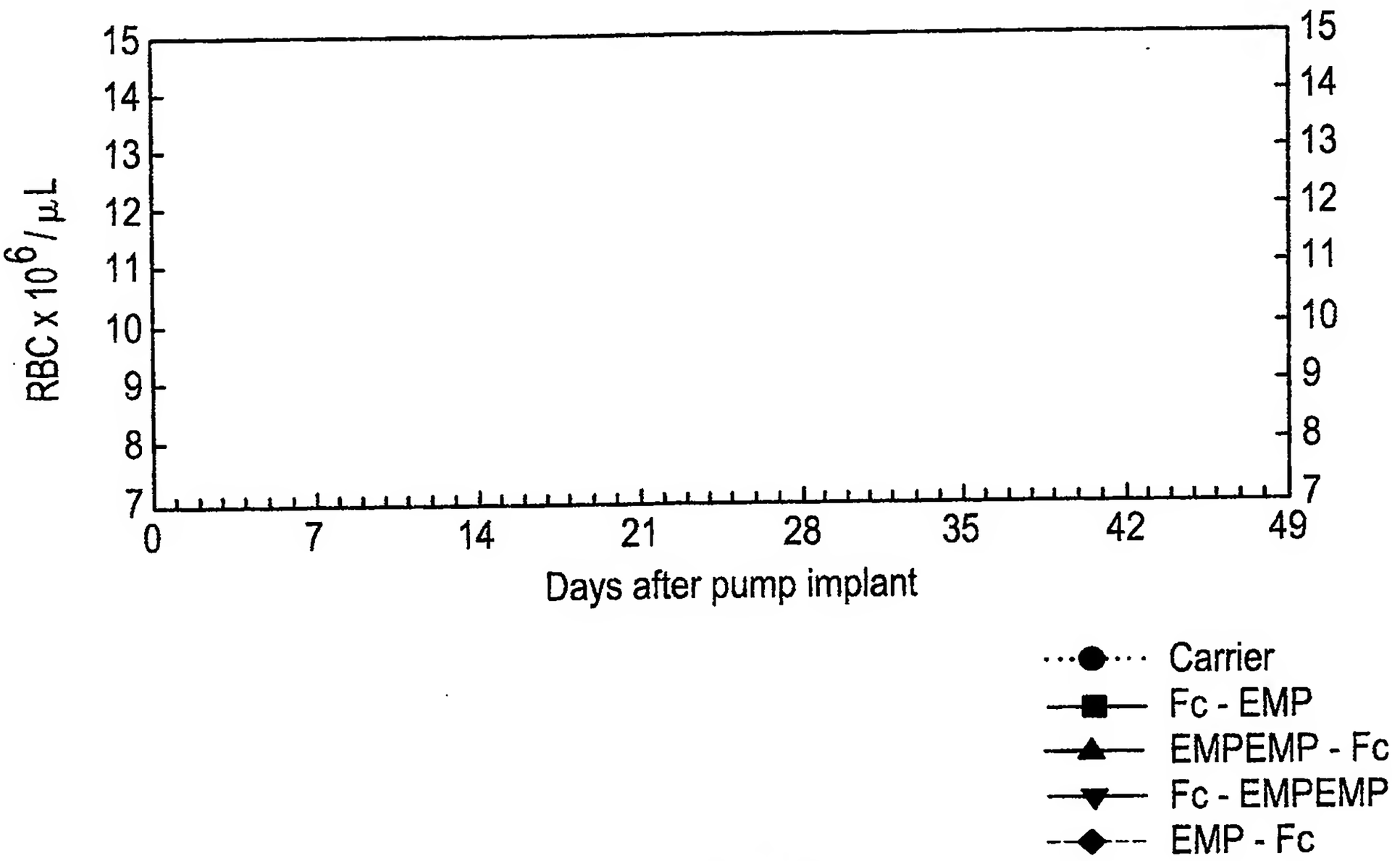


FIG.18B - 3

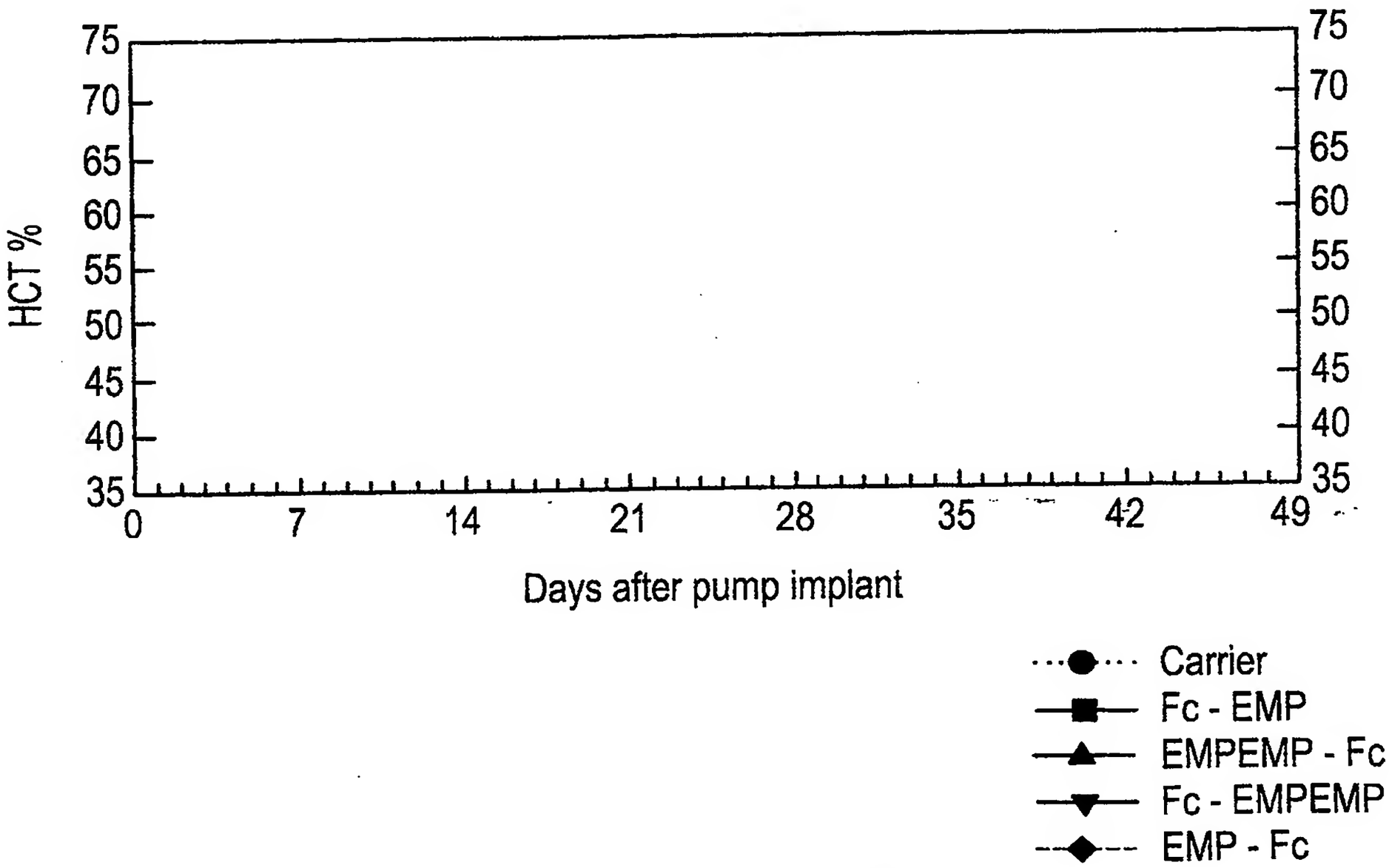


FIG. 19A

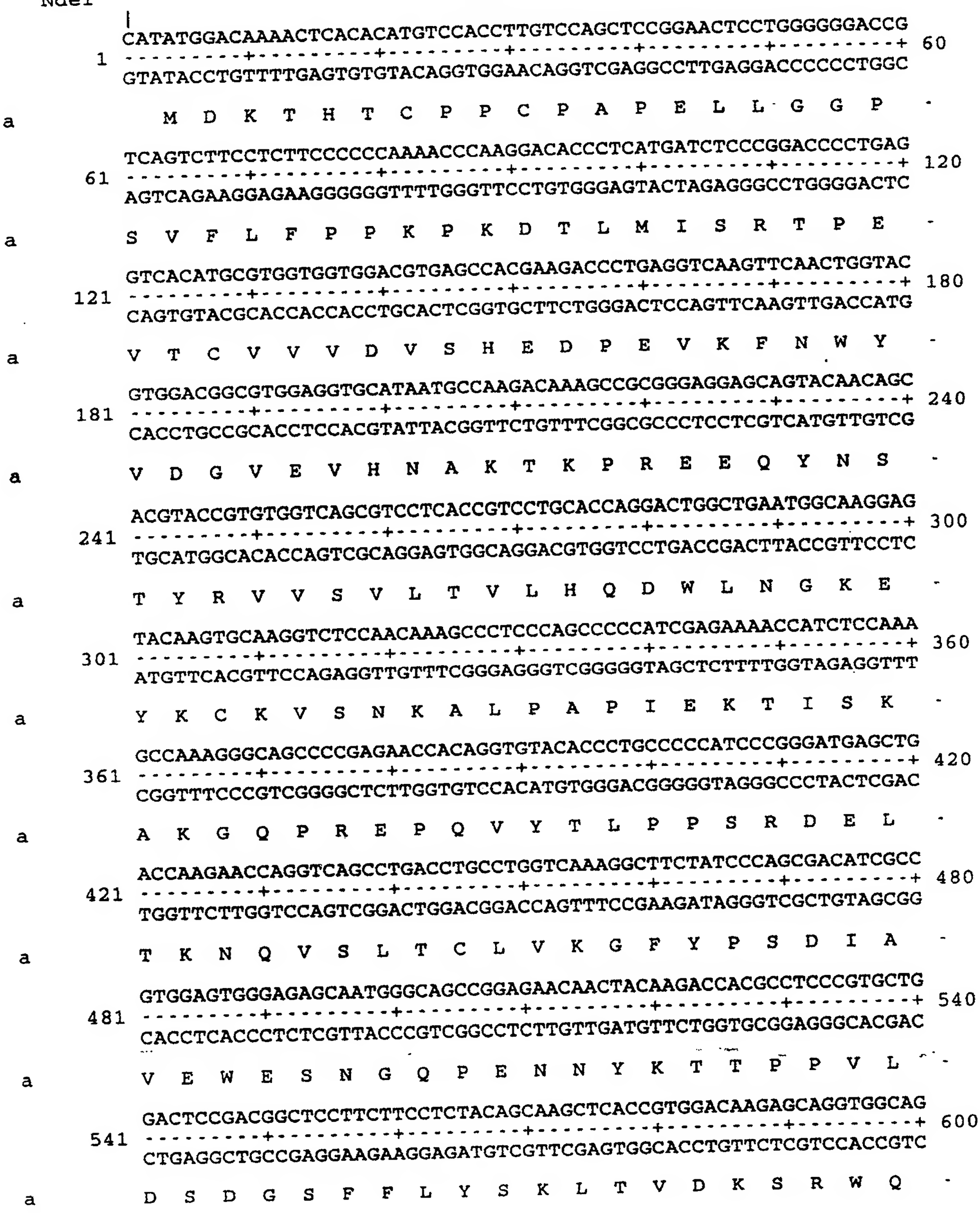

NdeI
CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
M D K T H T C P P C P A P E L L G G P
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
S V F L F P P K P K D T L M I S R T P E
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
V T C V V V D V S H E D P E V K F N W Y
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
V D G V E V H N A K T K P R E E Q Y N S
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
T Y R V V S V L T V L H Q D W L N G K E
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
Y K C K V S N K A L P A P I E K T I S K
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
A K G Q P R E P Q V Y T L P P S R D E L
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
T K N Q V S L T C L V K G F Y P S D I A
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
V E W E S N G Q P E N N Y K T T P P V L
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
D S D G S F F L Y S K L T V D K S R W Q

FIG. 19B

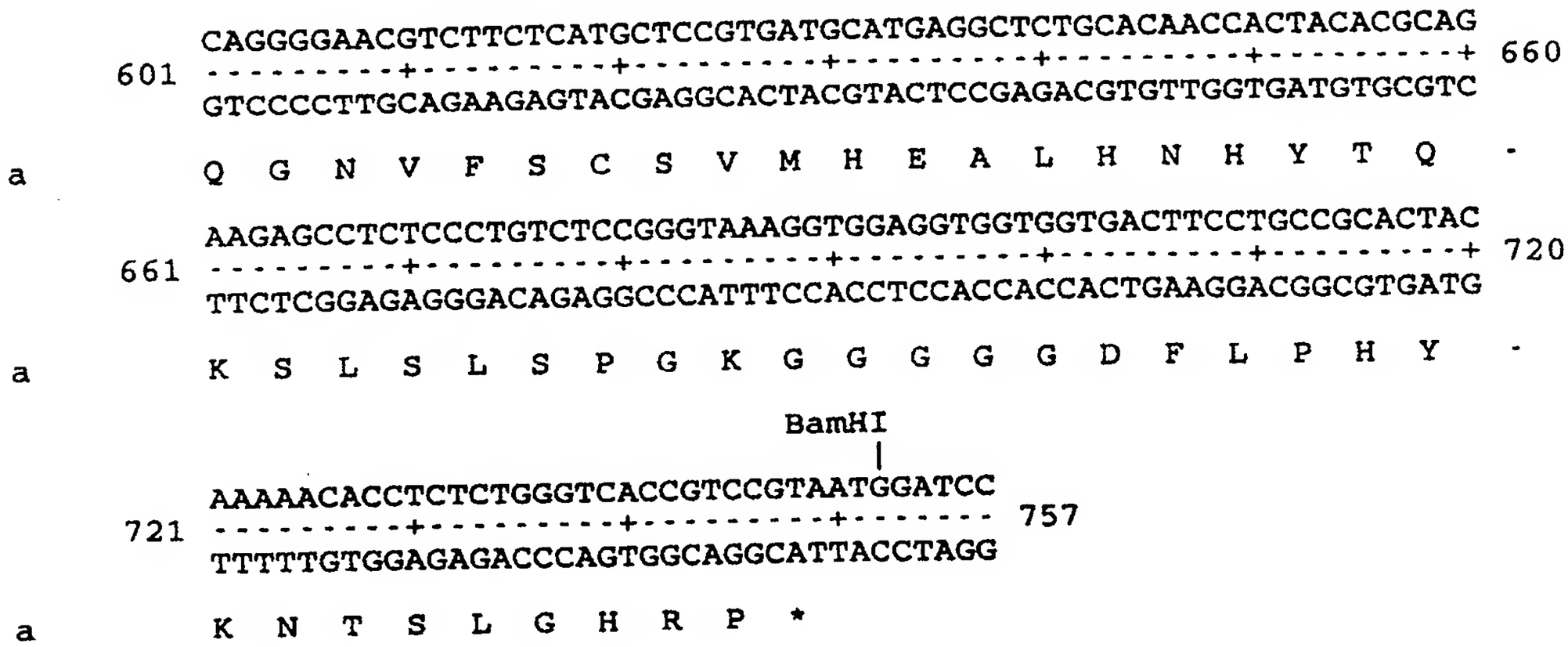

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 ---------+---------+---------+---------+---------+---------+---------+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
661 ---------+---------+---------+---------+---------+---------+---------+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG
a K S L S L S P G K G G G G G D F L P H Y -
BamHI
AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
721 ---------+---------+---------+-------- 757
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG
a K N T S L G H R P *

FIG. 20A

```
                NdeI
                 |
                CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTCACCGTCCGGGTGGAGGC
              1 ---------+---------+---------+---------+---------+---------+ 60
                GTATACCTGAAGGACGGCGTGATGTTTTTGTGGAGAGACCCAGTGGCAGGCCCACCTCCG

a                  M   D   F   L   P   H   Y   K   N   T   S   L   G   H   R   P   G   G   G   -

                GGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
             61 ---------+---------+---------+---------+---------+---------+ 120
                CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC

a                  G   G   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   P   -

                TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
            121 ---------+---------+---------+---------+---------+---------+ 180
                AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a                  S   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   -

                GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
            181 ---------+---------+---------+---------+---------+---------+ 240
                CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a                  V   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   -

                GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
            241 ---------+---------+---------+---------+---------+---------+ 300
                CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a                  V   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   -

                ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
            301 ---------+---------+---------+---------+---------+---------+ 360
                TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a                  T   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   -

                TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
            361 ---------+---------+---------+---------+---------+---------+ 420
                ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a                  Y   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   -

                GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
            421 ---------+---------+---------+---------+---------+---------+ 480
                CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a                  A   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   -

                ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
            481 ---------+---------+---------+---------+---------+---------+ 540
                TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a                  T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   -

                GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
            541 ---------+---------+---------+---------+---------+---------+ 600
                CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC

a                  V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   -
```

FIG. 20B


GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
601 ---------+---------+---------+---------+---------+---------+---------+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661 ---------+---------+---------+---------+---------+---------+---------+ 720
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
BamHI
AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
721 ---------+---------+---------+---------+---------+- 761
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC
a K S L S L S P G K *

FIG. 21A

```
                NdeI
                 |
                CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGGACCG
             1  ---------+---------+---------+---------+---------+---------+ 60
                GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a                  M   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   P   -

                TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
            61  ---------+---------+---------+---------+---------+---------+ 120
                AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a               S   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   -

                GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
           121  ---------+---------+---------+---------+---------+---------+ 180
                CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a               V   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   -

                GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
           181  ---------+---------+---------+---------+---------+---------+ 240
                CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a               V   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   -

                ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
           241  ---------+---------+---------+---------+---------+---------+ 300
                TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a               T   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   -

                TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
           301  ---------+---------+---------+---------+---------+---------+ 360
                ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a               Y   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   -

                GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
           361  ---------+---------+---------+---------+---------+---------+ 420
                CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a               A   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   -

                ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
           421  ---------+---------+---------+---------+---------+---------+ 480
                TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a               T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   -

                GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
           481  ---------+---------+---------+---------+---------+---------+ 540
                CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC

a               V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   -

                GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
           541  ---------+---------+---------+---------+---------+---------+ 600
                CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a               D   S   D   G   S   F   F   L   Y   S   K   L   T   V   D   K   S   R   W   Q   -
```

FIG. 21B

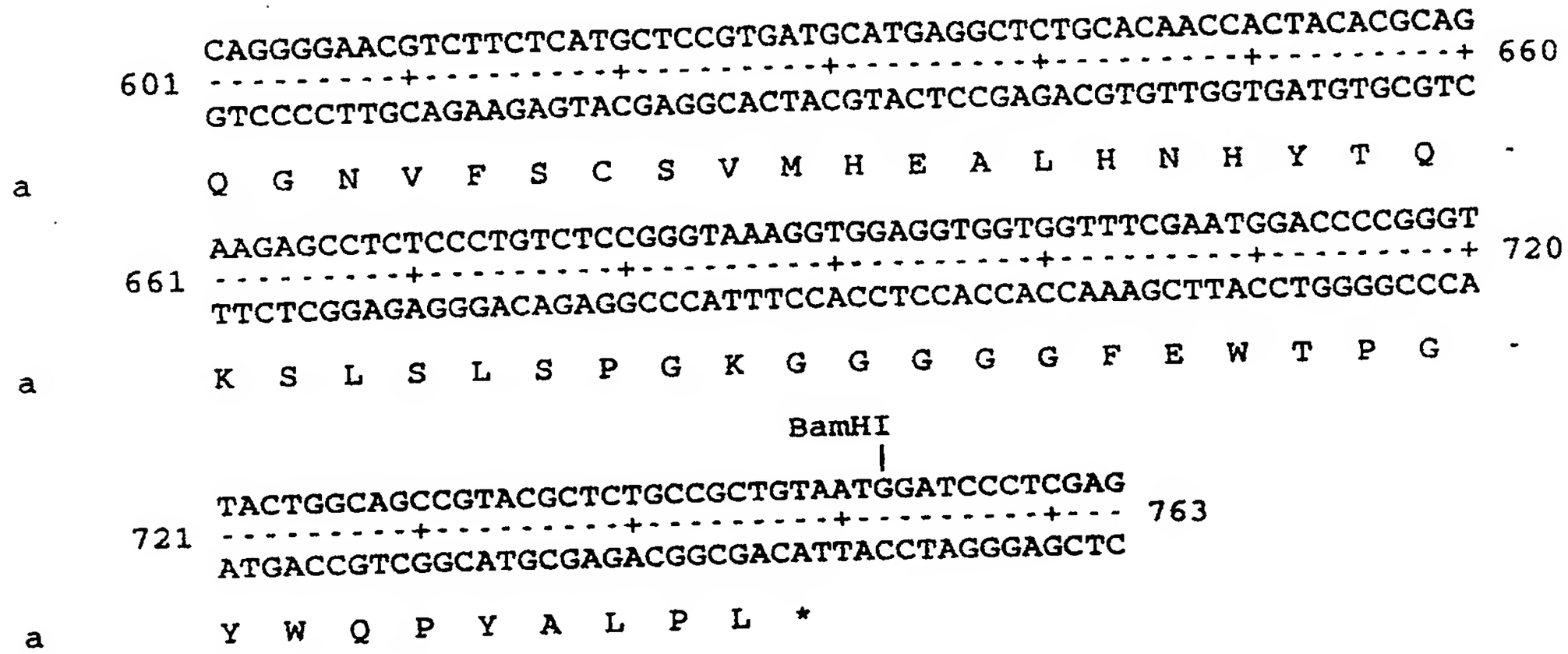

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 ----------+----------+----------+----------+----------+----------+---------- 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
661 ----------+----------+----------+----------+----------+----------+---------- 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA
a K S L S L S P G K G G G G G F E W T P G -
BamHI
TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
721 ----------+----------+----------+----------+----------+--- 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC
a Y W Q P Y A L P L *

FIG. 22A

```
                NdeI
                 |
                CATATGTTCGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC
          1     ---------+---------+---------+---------+---------+---------+ 60
                GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG

a                  M   F   E   W   T   P   G   Y   W   Q   P   Y   A   L   P   L   G   G   G   -

                GGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
         61     ---------+---------+---------+---------+---------+---------+ 120
                CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC

a                  G   G   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   P   -

                TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
        121     ---------+---------+---------+---------+---------+---------+ 180
                AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a                  S   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   -

                GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
        181     ---------+---------+---------+---------+---------+---------+ 240
                CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a                  V   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   -

                GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
        241     ---------+---------+---------+---------+---------+---------+ 300
                CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a                  V   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   -

                ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
        301     ---------+---------+---------+---------+---------+---------+ 360
                TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a                  T   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   -

                TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
        361     ---------+---------+---------+---------+---------+---------+ 420
                ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a                  Y   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   -

                GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
        421     ---------+---------+---------+---------+---------+---------+ 480
                CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a                  A   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   -

                ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
        481     ---------+---------+---------+---------+---------+---------+ 540
                TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a                  T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   -

                GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
        541     ---------+---------+---------+---------+---------+---------+ 600
                CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC

a                  V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   -
```

FIG. 22B


GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
601 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661 720
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
BamHI
AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 757
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a K S L S L S P G K *

FIG. 23A

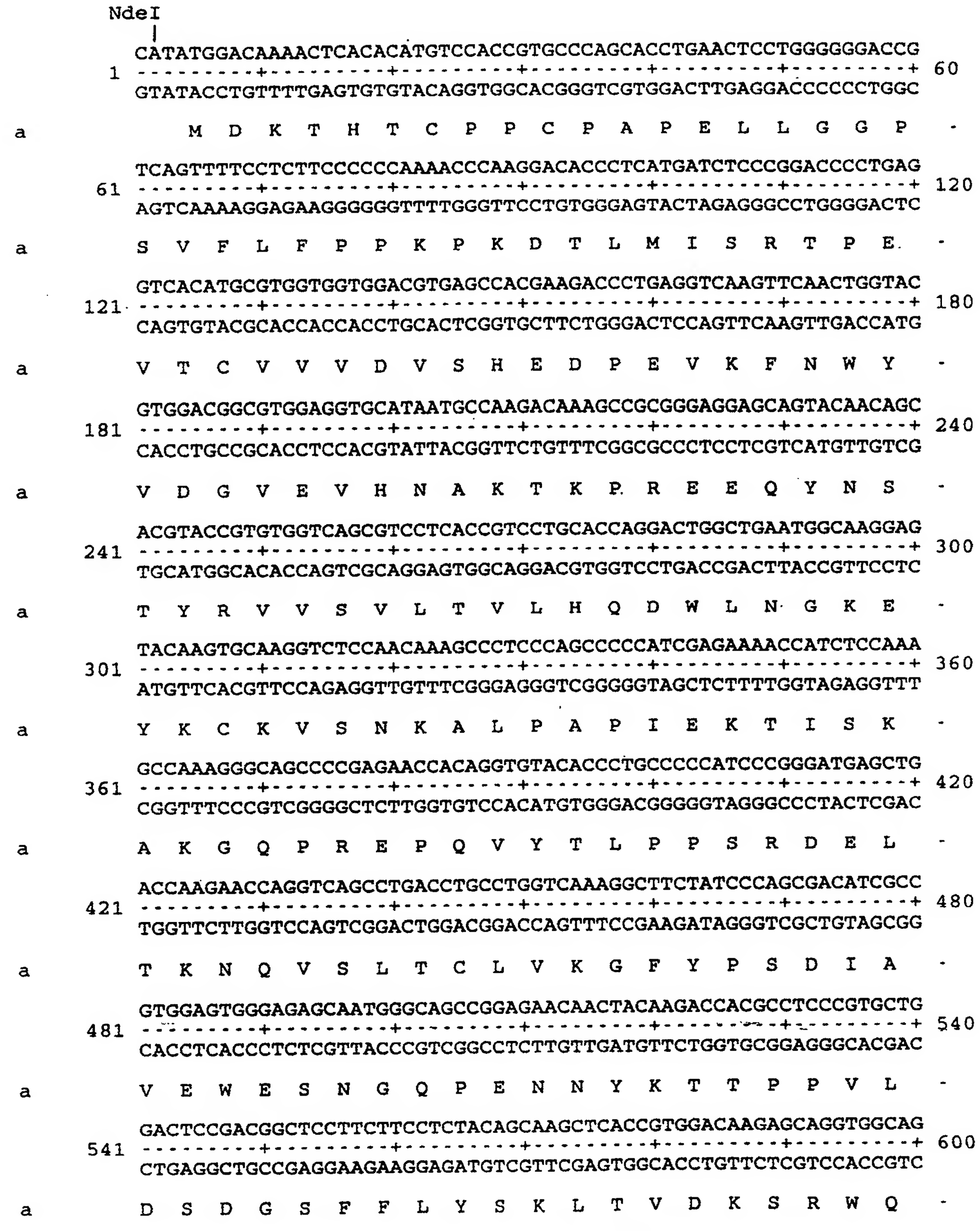

NdeI
CATATGGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 23B

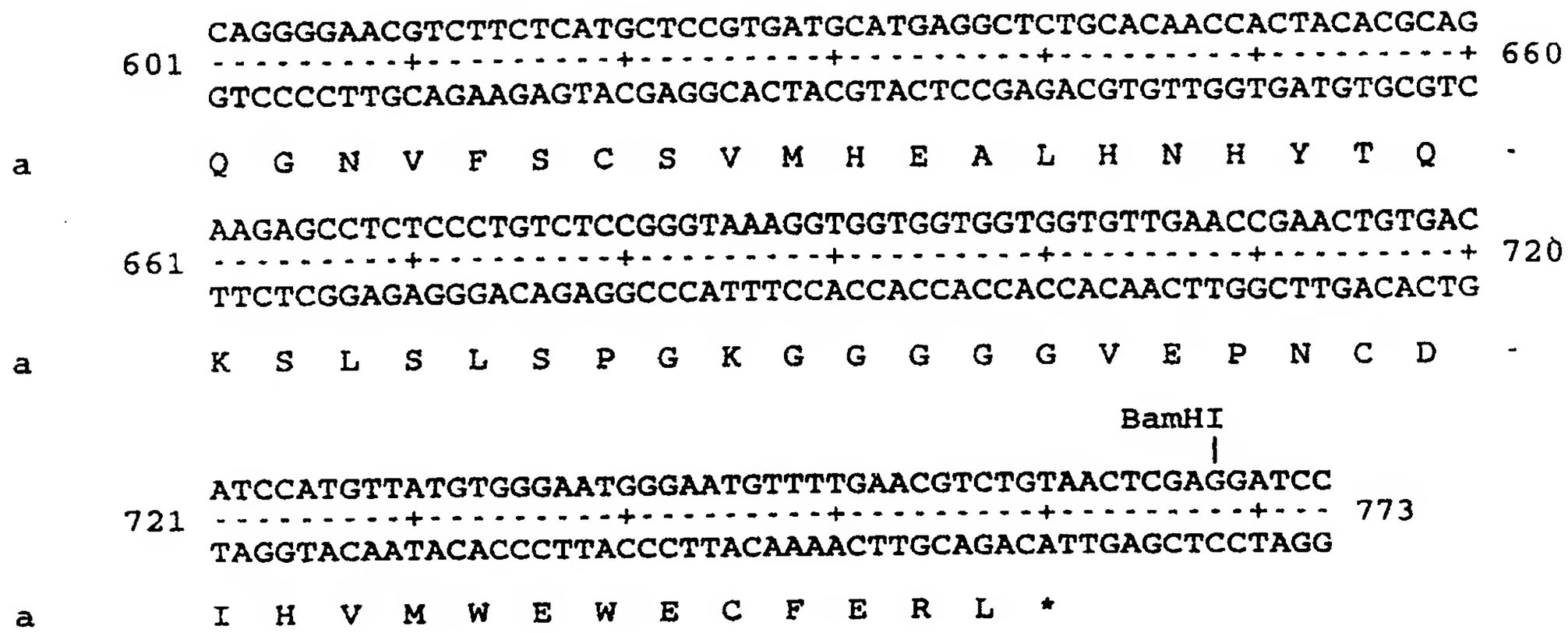

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 ----------+----------+----------+----------+----------+----------+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGTTGAACCGAACTGTGAC
661 ----------+----------+----------+----------+----------+----------+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACTTGGCTTGACACTG
a K S L S L S P G K G G G G G V E P N C D -
BamHI
ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACTCGAGGATCC
721 ----------+----------+----------+----------+----------+---- 773
TAGGTACAATACACCCTTACCCTTACAAAACTTGCAGACATTGAGCTCCTAGG
a I H V M W E W E C F E R L *

FIG. 24A

```
          NdeI
            |
            CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
          1 ---------+---------+---------+---------+---------+---------+---------+ 60
            GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACTTGCA

a                M   V   E   P   N   C   D   I   H   V   M   W   E   W   E   C   F   E   R   -

            CTGGGTGGTGGTGGTGGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTC
         61 ---------+---------+---------+---------+---------+---------+---------+ 120
            GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG

a                L   G   G   G   G   G   D   K   T   H   T   C   P   P   C   P   A   P   E   L   -

            CTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC
        121 ---------+---------+---------+---------+---------+---------+---------+ 180
            GACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG

a                L   G   G   P   S   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   -

            CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
        181 ---------+---------+---------+---------+---------+---------+---------+ 240
            GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

a                R   T   P   E   V   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   -

            TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
        241 ---------+---------+---------+---------+---------+---------+---------+ 300
            AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

a                F   N   W   Y   V   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   -

            CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
        301 ---------+---------+---------+---------+---------+---------+---------+ 360
            GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC

a                Q   Y   N   S   T   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   -

            AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
        361 ---------+---------+---------+---------+---------+---------+---------+ 420
            TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT

a                N   G   K   E   Y   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   -

            ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
        421 ---------+---------+---------+---------+---------+---------+---------+ 480
            TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG

a                T   I   S   K   A   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   -

            CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
        481 ---------+---------+---------+---------+---------+---------+---------+ 540
            GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG

a                R   D   E   L   T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   -

            AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG
        541 ---------+---------+---------+---------+---------+---------+---------+ 600
            TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC

a                S   D   I   A   V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   -
```

FIG. 24B

```
    CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG
601 ---------+---------+---------+---------+---------+---------+---------+ 660
    GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC

a       P   P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L   T   V   D   K   -

    AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
661 ---------+---------+---------+---------+---------+---------+---------+ 720
    TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG

a       S   R   W   Q   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   -

                                                          BamHI
                                                            |
    CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
721 ---------+---------+---------+---------+---------+---------+--- 773
    GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG

a       H   Y   T   Q   K   S   L   S   L   S   P   G   K   *
```

FIG. 25A

```
          NdeI
            |
            CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG
          1 ---------+---------+---------+---------+---------+---------+---------+ 60
            GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC

a                M   D   K   T   H   T   C   P   P   C   P   A   P   E   L   L   G   G   P   -

            TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
         61 ---------+---------+---------+---------+---------+---------+---------+ 120
            AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a                S   V   F   L   F   P   P   K   P   K   D   T   L   M   I   S   R   T   P   E   -

            GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
        121 ---------+---------+---------+---------+---------+---------+---------+ 180
            CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a                V   T   C   V   V   V   D   V   S   H   E   D   P   E   V   K   F   N   W   Y   -

            GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
        181 ---------+---------+---------+---------+---------+---------+---------+ 240
            CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG

a                V   D   G   V   E   V   H   N   A   K   T   K   P   R   E   E   Q   Y   N   S   -

            ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
        241 ---------+---------+---------+---------+---------+---------+---------+ 300
            TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a                T   Y   R   V   V   S   V   L   T   V   L   H   Q   D   W   L   N   G   K   E   -

            TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
        301 ---------+---------+---------+---------+---------+---------+---------+ 360
            ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a                Y   K   C   K   V   S   N   K   A   L   P   A   P   I   E   K   T   I   S   K   -

            GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
        361 ---------+---------+---------+---------+---------+---------+---------+ 420
            CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a                A   K   G   Q   P   R   E   P   Q   V   Y   T   L   P   P   S   R   D   E   L   -

            ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
        421 ---------+---------+---------+---------+---------+---------+---------+ 480
            TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a                T   K   N   Q   V   S   L   T   C   L   V   K   G   F   Y   P   S   D   I   A   -

            GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
        481 ---------+---------+---------+---------+---------+---------+---------+ 540
            CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC

a                V   E   W   E   S   N   G   Q   P   E   N   N   Y   K   T   T   P   P   V   L   -

            GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
        541 ---------+---------+---------+---------+---------+---------+---------+ 600
            CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a                D   S   D   G   S   F   F   L   Y   S   K   L   T   V   D   K   S   R   W   Q   -
```

FIG. 25B

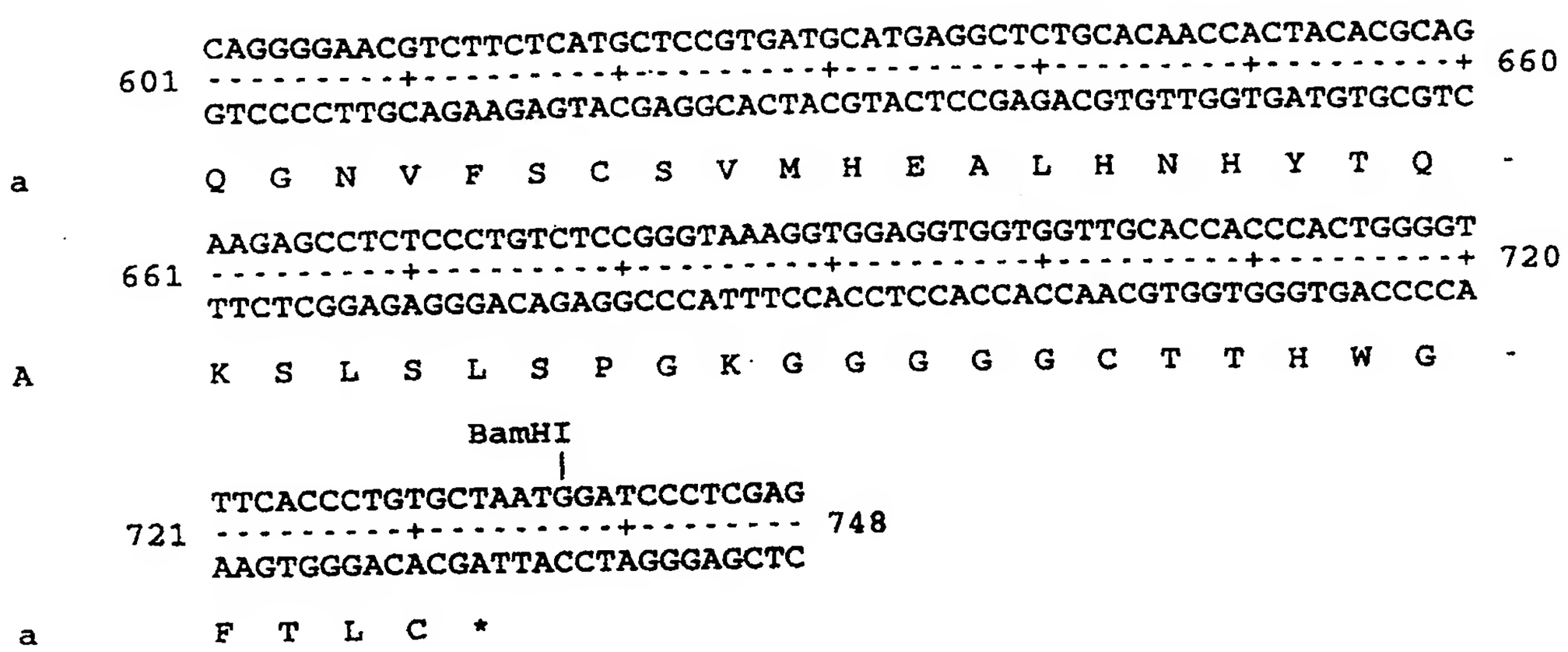

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
601 ---------+---------+---------+---------+---------+---------+ 660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
661 ---------+---------+---------+---------+---------+---------+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA
A K S L S L S P G K G G G G G C T T H W G -
BamHI
TTCACCCTGTGCTAATGGATCCCTCGAG
721 ---------+---------+--------- 748
AAGTGGGACACGATTACCTAGGGAGCTC
a F T L C *

FIG. 26A

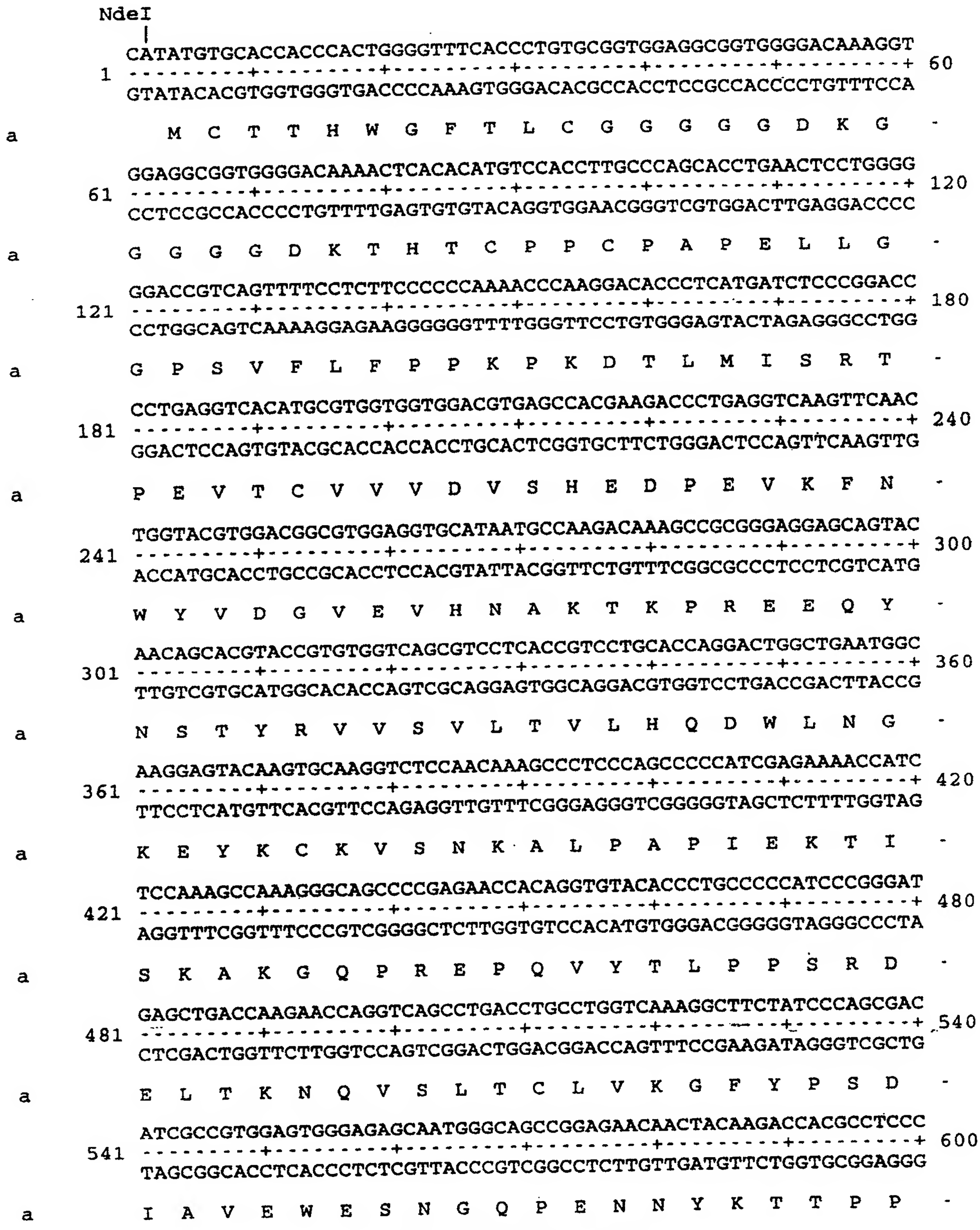
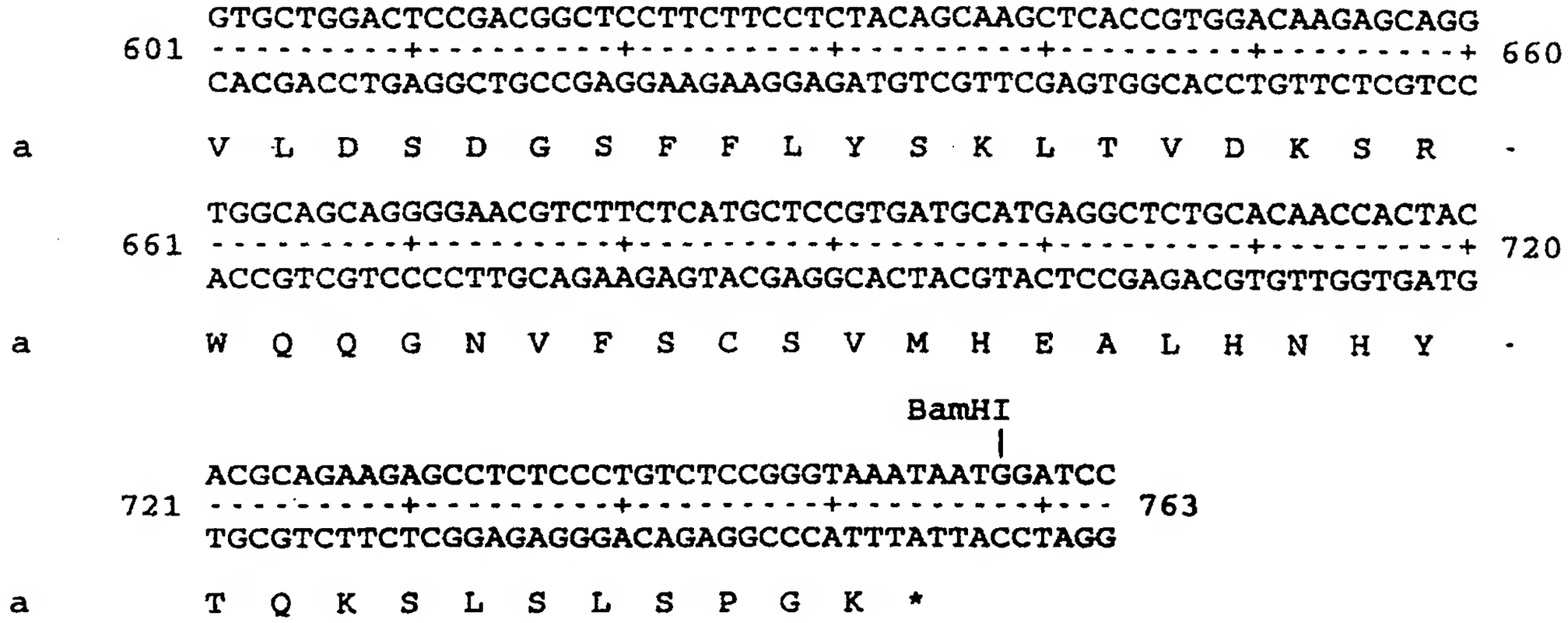

NdeI
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT
1 ---------+---------+---------+---------+---------+---------+ 60
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA
a M C T T H W G F T L C G G G G G D K G -
GGAGGCGGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG
61 ---------+---------+---------+---------+---------+---------+ 120
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCC
a G G G G D K T H T C P P C P A P E L L G -
GGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
121 ---------+---------+---------+---------+---------+---------+ 180
CCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG
a G P S V F L F P P K P K D T L M I S R T -
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
181 ---------+---------+---------+---------+---------+---------+ 240
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG
a P E V T C V V V D V S H E D P E V K F N -
TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
241 ---------+---------+---------+---------+---------+---------+ 300
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG
a W Y V D G V E V H N A K T K P R E E Q Y -
AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
301 ---------+---------+---------+---------+---------+---------+ 360
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG
a N S T Y R V V S V L T V L H Q D W L N G -
AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
361 ---------+---------+---------+---------+---------+---------+ 420
TTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG
a K E Y K C K V S N K A L P A P I E K T I -
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
421 ---------+---------+---------+---------+---------+---------+ 480
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA
a S K A K G Q P R E P Q V Y T L P P S R D -
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
481 ---------+---------+---------+---------+---------+---------+ 540
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG
a E L T K N Q V S L T C L V K G F Y P S D -
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCC
541 ---------+---------+---------+---------+---------+---------+ 600
TAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGG
a I A V E W E S N G Q P E N N Y K T T P P -

FIG. 26B


GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
601
660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCC
a V L D S D G S F F L Y S K L T V D K S R -
TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661
720
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a W Q Q G N V F S C S V M H E A L H N H Y -
BamHI
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721
763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a T Q K S L S L S P G K *